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* * * * * * * * * *   Welcome to STN International   * * * * * * * * * *

 NEWS  1           Web Page for STN Seminar Schedule - N. America
 NEWS  2  NOV 21   CAS patent coverage to include exemplified prophetic
                   substances identified in English-, French-, German-,
                   and Japanese-language basic patents from 2004-present
 NEWS  3  NOV 26   MARPAT enhanced with FSORT command
 NEWS  4  NOV 26   CHEMSAFE now available on STN Easy
 NEWS  5  NOV 26   Two new SET commands increase convenience of STN
                   searching
 NEWS  6  DEC 01   ChemPort single article sales feature unavailable
 NEWS  7  DEC 12   GBFULL now offers single source for full-text
                   coverage of complete UK patent families
 NEWS  8  DEC 17   Fifty-one pharmaceutical ingredients added to PS
 NEWS  9  JAN 06   The retention policy for unread STNmail messages
                   will change in 2009 for STN-Columbus and STN-Tokyo
 NEWS 10  JAN 07   WPIDS, WPINDEX, and WPIX enhanced Japanese Patent
                   Classification Data
 NEWS 11  FEB 02   Simultaneous left and right truncation (SLART) added
                   for CERAB, COMPUAB, ELCOM, and SOLIDSTATE
 NEWS 12  FEB 02   GENBANK enhanced with SET PLURALS and SET SPELLING
 NEWS 13  FEB 06   Patent sequence location (PSL) data added to USGENE
 NEWS 14  FEB 10   COMPENDEX reloaded and enhanced
 NEWS 15  FEB 11   WTEXTILES reloaded and enhanced
 NEWS 16  FEB 19   New patent-examiner citations in 300,000 CA/CAplus
                   patent records provide insights into related prior
                   art
 NEWS 17  FEB 19   Increase the precision of your patent queries -- use
                   terms from the IPC Thesaurus, Version 2009.01
 NEWS 18  FEB 23   Several formats for image display and print options
                   discontinued in USPATFULL and USPAT2
 NEWS 19  FEB 23   MEDLINE now offers more precise author group fields
                   and 2009 MeSH terms
 NEWS 20  FEB 23   TOXCENTER updates mirror those of MEDLINE - more
                   precise author group fields and 2009 MeSH terms
 NEWS 21  FEB 23   Three million new patent records blast AEROSPACE into
                   STN patent clusters
 NEWS 22  FEB 25   USGENE enhanced with patent family and legal status
                   display data from INPADOCDB
 NEWS 23  MAR 06   INPADOCDB and INPAFAMDB enhanced with new display
                   formats
 NEWS 24  MAR 11   EPFULL backfile enhanced with additional full-text
                   applications and grants
 NEWS 25  MAR 11   ESBIOBASE reloaded and enhanced

 NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,
              AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.

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 NEWS LOGIN    Welcome Banner and News Items
 NEWS IPC8     For general information regarding STN implementation of IPC 8

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FILE 'HOME' ENTERED AT 09:34:22 ON 12 MAR 2009

=> file medline
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COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                     0.22       0.22

FILE 'MEDLINE' ENTERED AT 09:34:30 ON 12 MAR 2009

 FILE LAST UPDATED: 11 Mar 2009 (20090311/UP).  FILE COVERS 1949 TO DATE.

 MEDLINE and LMEDLINE have been updated with the 2009 Medical Subject
 Headings (MeSH) vocabulary and tree numbers from the U.S.  National Library
 of Medicine (NLM).  Additional information is available at

 http://www.nlm.nih.gov/pubs/techbull/nd08/nd08_medline_data_changes_2009.html.

 On February 21, 2009, MEDLINE was reloaded.  See HELP RLOAD for details.

 This file contains CAS Registry Numbers for easy and accurate
 substance identification.

 See HELP RANGE before carrying out any RANGE search.

=> s resolv? and ambigu? and (name or entity) and (structure or architecture or object) and (
        102792 RESOLV?
         15644 AMBIGU?
         28758 NAME
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                 (NAME OR NAMES)
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        713700 STRUCTURE
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             6 LSID
                 (LSID OR LSIDS)
             8 GUID
L1           0 RESOLV? AND AMBIGU? AND (NAME OR ENTITY) AND (STRUCTURE OR ARCHI
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L2           6 RESOLV? AND AMBIGU? AND (NAME OR ENTITY) AND (STRUCTURE OR ARCHI
               TECTURE OR OBJECT)

=> d bib an 1-6

L2   ANSWER 1 OF 6     MEDLINE on STN
Full Text
AN   2008661253     MEDLINE
DN   PubMed ID: 18692976
TI   The All-Species Living Tree project: a 16S rRNA-based phylogenetic tree of
     all sequenced type strains.
AU   Yarza Pablo; Richter Michael; Peplies Jorg; Euzeby Jean; Amann Rudolf;
     Schleifer Karl-Heinz; Ludwig Wolfgang; Glockner Frank Oliver;
     Rossello-Mora Ramon
CS   Marine Microbiology Group, Institut Mediterrani d'Estudis Avancats
     (CSIC-UIB), C/ Miquel Marques 21, E-07190 Esporles, Illes Balears,
     Mallorca, Spain.
SO   Systematic and applied microbiology, (2008 Sep) Vol. 31, No. 4, pp.
     241-50.  Electronic Publication: 2008-08-09.
     Journal code: 8306133. ISSN: 0723-2020.
CY   Germany: Germany, Federal Republic of
DT   Journal; Article; (JOURNAL ARTICLE)
     (RESEARCH SUPPORT, NON-U.S. GOV'T)
LA   English
FS   Priority Journals
EM   200812
ED   Entered STN: 17 Oct 2008
     Last Updated on STN: 2 Jan 2009
     Entered Medline: 16 Dec 2008
AN   2008661253     MEDLINE

L2   ANSWER 2 OF 6     MEDLINE on STN
Full Text
AN   2008508769     MEDLINE
DN   PubMed ID: 18689813
TI   Inter-species normalization of gene mentions with GNAT.
AU   Hakenberg Jorg; Plake Conrad; Leaman Robert; Schroeder Michael; Gonzalez
     Graciela
CS   Department of Computer Science and Engineering, Arizona State University,
     Tempe, AZ 85287, USA.. joerg.hakenberg@asu.edu
SO   Bioinformatics (Oxford, England), (2008 Aug 15) Vol. 24, No. 16, pp.
     i126-132.
     Journal code: 9808944. E-ISSN: 1460-2059.
CY   England: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200810
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ED Entered STN: 12 Aug 2008
Last Updated on STN: 21 Oct 2008
Entered Medline: 20 Oct 2008
AN 2008508769 MEDLINE

L2 ANSWER 3 OF 6 MEDLINE on STN
Full Text
AN 2007193000 MEDLINE
DN PubMed ID: 17394580
TI Children's questions: a mechanism for cognitive development.
AU Chouinard Michael M
CS Department of SSHA, University of California, Merced, CA 95344, USA.. mchouinard@ucmerced.edu
SO Monographs of the Society for Research in Child Development, (2007) Vol. 72, No. 1, pp. vii-ix, 1-112; discussion 113-26.
Journal code: 7508397. ISSN: 0037-976X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, N.I.H., EXTRAMURAL)
LA English
FS Priority Journals
EM 200706
ED Entered STN: 31 Mar 2007
Last Updated on STN: 28 Jun 2007
Entered Medline: 27 Jun 2007
AN 2007193000 MEDLINE

L2 ANSWER 4 OF 6 MEDLINE on STN
Full Text
AN 2007050471 MEDLINE
DN PubMed ID: 17254295
TI NERBio: using selected word conjunctions, term normalization, and global patterns to improve biomedical named **entity** recognition.
AU Tsai Richard Tzong-Han; Sung Cheng-Lung; Dai Hong-Jie; Hung Hsieh-Chuan; Sung Ting-Yi; Hsu Wen-Lian
CS Institute of Information Science, Academia Sinica, Nankang, Taipei 115, Taiwan, Republic of China.. thtsai@iis.sinica.edu.tw
SO BMC bioinformatics, (2006) Vol. 7 Suppl 5, pp. S11. Electronic Publication: 2006-12-18.
Journal code: 100965194. E-ISSN: 1471-2105.
Report No.: NLM-PMC1764467.
CY England: United Kingdom
DT (EVALUATION STUDIES)
Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 200704
ED Entered STN: 27 Jan 2007
Last Updated on STN: 27 Apr 2007
Entered Medline: 26 Apr 2007
AN 2007050471 MEDLINE

L2 ANSWER 5 OF 6 MEDLINE on STN
Full Text
AN 2005695098 MEDLINE
DN PubMed ID: 16382832
TI The Microbial Rosetta Stone database: A common **structure** for microbial biosecurity threat agents.
AU Ecke David J; Sampath Rangarajan; Willett Paul; Samant Vivek; Massire Christian; Hall Thomas A; Hari Kumar; McNeil John A; Buchen-Osmond Cornelia; Budowle Bruce
CS Ibis Division of Isis Pharmaceuticals, 1891 Rutherford Rd., Carlsbad, CA 92008, USA.
SO Journal of forensic sciences, (2005 Nov) Vol. 50, No. 6, pp. 1380-5.
Journal code: 0375370. ISSN: 0022-1198.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, U.S. GOV'T, NON-P.H.S.)
LA English
FS Priority Journals
EM 200602

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ED   Entered STN: 31 Dec 2005
     Last Updated on STN: 8 Feb 2006
     Entered Medline: 7 Feb 2006
AN   2005695098     MEDLINE

L2   ANSWER 6 OF 6     MEDLINE on STN
Full Text
AN   2004531610     MEDLINE
DN   PubMed ID: 15502395
TI   A new mechanosensitive channel SAKCA and a new MS channel blocker GsTMx-4.
AU   Sokabe Masahiro; Naruse Keiji; Qiong-Yao Tang
CS   Department of Physiology, Nagoya University Graduate School of Medicine.
SO   Nippon yakurigaku zasshi. Folia pharmacologica Japonica, (2004 Nov) Vol.
     124, No. 5, pp. 301-10.  Ref: 40
     Journal code: 0420550. ISSN: 0015-5691.
CY   Japan
DT   (ENGLISH ABSTRACT)
     (IN VITRO)
     Journal; Article; (JOURNAL ARTICLE)
     General Review; (REVIEW)
LA   Japanese
FS   Priority Journals
EM   200502
ED   Entered STN: 26 Oct 2004
     Last Updated on STN: 1 Mar 2005
     Entered Medline: 25 Feb 2005
AN   2004531610     MEDLINE


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         43562 ENTITY
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                  (ENTITY OR ENTITIES)
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L3          11 RESOLV? AND AMBIGU? AND (NAME OR ENTITY OR TAXON? OR METADATA)
               AND (STRUCTURE OR ARCHITECTURE OR OBJECT)

=> s l3 not l2
L4           5 L3 NOT L2

=> d bib ab 1-5

L4   ANSWER 1 OF 5     MEDLINE on STN
Full Text
AN   2008664110     MEDLINE
DN   PubMed ID: 18675585
TI   Analysis of the internal transcribed spacer 2 (ITS2) region of
     scuticociliates and related taxa (Ciliophora, Oligohymenophorea) to infer
     their evolution and phylogeny.
AU   Miao Miao; Warren Alan; Song Weibo; Wang Shi; Shang Huimin; Chen Zigui
CS   Laboratory of Protozoology, Ocean University of China, Qingdao 266003,
     China.
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SO Protist, (2008 Oct) Vol. 159, No. 4, pp. 519-33.
Journal code: 9806488. ISSN: 1434-4610.
CY Germany: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200812
ED Entered STN: 18 Oct 2008
Last Updated on STN: 2 Jan 2009
Entered Medline: 16 Dec 2008
AB The ITS2 (ITS--internal transcribed spacer) region of the rDNA in 11 representative scuticociliates and two **ambiguously** related genera was analyzed. In common with other eukaryotes, the putative ITS2 folding pattern consists of a closed loop with four helices supported by minimum free energy and compensatory base changes (CBCs), although two of these helices are variable and sometimes absent. Three topologies were obtained on the basis of traditional primary sequence analysis, "string" strategy of secondary **structure** and analysis of the combined data. It was found that the secondary **structure** information could help to improve alignment and utilize appropriately phylogenetic strategies. The proposed phylogenies, though differing between sequence- and **structure**-based results, provide consistent support for high-level clades: the systematically questionable genera Dexiotrichides and Cardiostomatella always cluster together in a clade basal to the scuticociliates s.s., whereas Pleuronema branches from other uronematids at a deep level, and is hence a divergent **taxon**. Within the well-supported monophyletic philasterids, a sister relationship exists between Orchitophrya and Mesanophrys, while Uronema shows a close relationship with the group including Paranophrys and Parauronema. The positions of Metanophrys, Pseudocohnilembus and Anophryoides among the philasterids remain poorly **resolved**. Our findings firmly support the proposed evolutionary scenario inferred previously both from morphological and molecular data.

L4 ANSWER 2 OF 5 MEDLINE on STN
Full Text
AN 2008532719 MEDLINE
DN PubMed ID: 18655698
TI ITS2 data corroborate a monophyletic chlorophycean DO-group (Sphaeropleales).
AU Keller Alexander; Schleicher Tina; Forster Frank; Ruderisch Benjamin; Dandekar Thomas; Muller Tobias; Wolf Matthias
CS Department of Bioinformatics, University of Wurzburg, Am Hubland, 97074 Wurzburg, Germany.. a.keller@biozentrum.uni-wuerzburg.de
SO BMC evolutionary biology, (2008) Vol. 8, pp. 218. Electronic Publication: 2008-07-25.
Journal code: 100966975. E-ISSN: 1471-2148.
Report No.: NLM-PMC2519086.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 200809
ED Entered STN: 26 Aug 2008
Last Updated on STN: 18 Sep 2008
Entered Medline: 17 Sep 2008
AB BACKGROUND: Within Chlorophyceae the ITS2 secondary **structure** shows an unbranched helix I, except for the 'Hydrodictyon' and the 'Scenedesmus' clade having a ramified first helix. The latter two are classified within the Sphaeropleales, characterised by directly opposed basal bodies in their flagellar apparatuses (DO-group). Previous studies could not **resolve** the **taxonomic** position of the 'Sphaeroplea' clade within the Chlorophyceae without **ambiguity** and two pivotal questions remain open: (1) Is the DO-group monophyletic and (2) is a branched helix I an apomorphic feature of the DO-group? In the present study we analysed the secondary **structure** of three newly obtained ITS2 sequences classified within the 'Sphaeroplea' clade and **resolved** sphaeroplealean relationships by applying different phylogenetic approaches based on a combined sequence-**structure** alignment. RESULTS: The newly obtained ITS2 sequences of Ankyra judayi, Atractomorpha porcata and Sphaeroplea annulina of the 'Sphaeroplea' clade do not show any branching in the secondary **structure** of their helix I. All applied phylogenetic methods highly

support the 'Sphaeroplea' clade as a sister group to the 'core Sphaeropleales'. Thus, the DO-group is monophyletic. Furthermore, based on characteristics in the sequence-**structure** alignment one is able to distinguish distinct lineages within the green algae. CONCLUSION: In green algae, a branched helix I in the secondary **structure** of the ITS2 evolves past the 'Sphaeroplea' clade. A branched helix I is an apomorph characteristic within the monophyletic DO-group. Our results corroborate the fundamental relevance of including the secondary **structure** in sequence analysis and phylogenetics.

L4 ANSWER 3 OF 5 MEDLINE on STN
Full Text
AN 2002164747 MEDLINE
DN PubMed ID: 11846600
TI Using the volumetric indices of telencephalic **structures** to distinguish Salamandridae and Plethodontidae: comparison of three statistical methods.
AU Dore Jean-Christophe; Ojasoo Tiil; Thireau Michel
CS Laboratoire des Substances Naturelles, ESA 8041 CNRS, Museum national d'Histoire naturelle, 63 rue Buffon, 75005 Paris, France.. dore@mnhn.fr
SO Journal of theoretical biology, (2002 Feb 7) Vol. 214, No. 3, pp. 427-39. Journal code: 0376342. ISSN: 0022-5193.
CY England: United Kingdom
DT (COMPARATIVE STUDY)
Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200204
ED Entered STN: 19 Mar 2002
Last Updated on STN: 20 Apr 2002
Entered Medline: 19 Apr 2002
AB The aim of this study was to establish whether appropriate statistical analysis of 16 volumetric indices corresponding to 16 **structures** making up the entire telencephalon of Urodela could distinguish between two families, Salamandridae and Plethodontidae. We compared the efficiency of three statistical methods (stepwise discriminant analysis, artificial neural networks, correspondence factor analysis) and the information they provide. All three methods found the same species difficult to classify. However, only correspondence factor analysis could suggest explanations for "misclassifications" as it superimposes the two sets of variables, (sub)species and anatomical variables, thus revealing the correlations between them. The bulbus olfactorius accessorius and the caudal mitral cell layer of the bulbus olfactorius principalis were the most discriminatory **structures** in separating Salamandridae and Plethodontidae. The correspondence factor analysis mapped species very much in line with accepted **taxonomy** and highlighted several current controversies [e.g. positioning of certain newts (T. marmoratus, T. vulgaris, T. alpestris), of Salamandrina terdigitata, and of members of the genus Euproctus]. Mapping of Plethodontidae was less clear-cut than that of Salamandridae with more overlap among genera but was quite consistent with knowledge of brain **structure** complexification. We conclude that relationships derived from analyses of telencephalic **structures** provide valuable information that might help **resolve ambiguities**; we have coined the term "neurotaxonomy" for this approach. Copyright 2002 Elsevier Science Ltd.

L4 ANSWER 4 OF 5 MEDLINE on STN
Full Text
AN 2000121754 MEDLINE
DN PubMed ID: 10658667
TI Phylogenetic relationships of Pleurotus species according to the sequence and secondary **structure** of the mitochondrial small-subunit rRNA V4, V6 and V9 domains.
AU Gonzalez P; Labarere J
CS Laboratory of Molecular Genetics and Breeding of Cultivated Mushrooms, INRA-University Victor Segalen Bordeaux, Villenave dOrnon, France.. labarere@bordeaux.inra.fr
SO Microbiology (Reading, England), (2000 Jan) Vol. 146 (Pt 1), pp. 209-21. Journal code: 9430468. ISSN: 1350-0872.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English

FS Priority Journals
OS GENBANK-AF091891; GENBANK-AF091892; GENBANK-AF091893; GENBANK-AF091894; GENBANK-AF091895; GENBANK-AF091896; GENBANK-AF091897; GENBANK-AF091898; GENBANK-AF091899; GENBANK-AF091900; GENBANK-AF091901; GENBANK-AF091902; GENBANK-AF091903; GENBANK-AF091904; GENBANK-AF091905; GENBANK-AF091906; GENBANK-AF091907; GENBANK-AF091908; GENBANK-AF091909; GENBANK-AF091910; GENBANK-AF091911; GENBANK-AF091912; GENBANK-AF091913; GENBANK-AF091914; GENBANK-AF091915; GENBANK-AF091916; GENBANK-AF091917; GENBANK-AF091918; GENBANK-AF091919; GENBANK-AF091920; +
EM 200003
ED Entered STN: 20 Mar 2000
Last Updated on STN: 20 Mar 2000
Entered Medline: 6 Mar 2000
AB A comparative study of the V4, V6 and V9 domains of the mitochondrial small-subunit (SSU) rRNA was conducted to evaluate the use of these sequences to investigate phylogenetic relatedness within the genus Pleurotus. The PCR products encompassing these regions from 48 isolates belonging to 16 Pleurotus species were sequenced and compared. From this comparison, the length and sequence of the three domains were found to be constant within a species. Significant inter-species variations due to insertion/deletion events were found, in most cases occurring in regions not directly involved in the maintainance of the standard SSU rRNA secondary **structure**. Phylogenetic analysis based upon these mitochondrial sequences was in agreement with relationships previously established by morphological descriptions and with previous studies based upon the nuclear genome or isozymes; moreover such analysis **resolved** some **ambiguities** in earlier analyses. It was confirmed that P. ostreatus and P. florida represent a single species, as well as P. pulmonarius and P. sajor-caju. The phylogenetic analysis also made it possible to assess the relative positions of P. rattenburyi, P. lampas, P. sapidus, P. colombinus and P. eryngii. The results clearly showed that sequences of the V4, V6 and V9 domains of the mitochondrial SSU rRNA could provide good markers for use in the **taxonomy** and phylogeny of species of Basidiomycota. Because of their nucleotide conservation, the major advantage of these species-specific markers was the possibility to study only one isolate from each species to determine phylogenetic relatedness.

L4 ANSWER 5 OF 5 MEDLINE on STN
Full Text
AN 1995211273 MEDLINE
DN PubMed ID: 7697190
TI Multiple origins of colonial green flagellates from unicells: evidence from molecular and organismal characters.
AU Buchheim M A; McAuley M A; Zimmer E A; Theriot E C; Chapman R L
CS Faculty of Biological Science, University of Tulsa, Oklahoma 74104-3189.
SO Molecular phylogenetics and evolution, (1994 Dec) Vol. 3, No. 4, pp. 322-43.
Journal code: 9304400. ISSN: 1055-7903.
CY United States
DT (COMPARATIVE STUDY)
Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
(RESEARCH SUPPORT, U.S. GOV'T, NON-P.H.S.)
LA English
FS Priority Journals
EM 199504
ED Entered STN: 10 May 1995
Last Updated on STN: 10 May 1995
Entered Medline: 28 Apr 1995
AB Phylogenetic hypotheses generated from cladistic analysis of organismal and molecular data are shown to be generally congruent and/or complementary for comparisons of unicellular and colonial green algae in the Chlorophyceae. Cladistic analysis of organismal character data corroborates the alliance of colonial Stephanosphaera with unicellular Haematococcus (Haematococcaceae sensu Smith), inferred from previous studies of nuclear-encoded rRNA sequence data. The organismal data also support monophyly of the colonial Volvocaceae (sensu Smith). Alliances of other unicellular taxa, including those ascribed to the "Euchlamydomonas" Hauptgruppe (sensu Ettl), are not **resolved** by organismal characters principally because the **structure** of the data is skewed to shared ancestral characters (symplesiomorphies) and unique characters (autapomorphies) which define individual taxa only. Reanalysis of rRNA

sequence data, with additional sequence data for critical taxa, does not support monophyly of the colonial Volvocaceae (sensu Smith). However, these data are weak in the support of the alternate hypothesis of nonmonophyly. In contrast, relationships among most unicellular flagellates are unambiguously **resolved** by the molecular data. Although the failure of the sequence data to **resolve** relationships among colonial flagellates appears to be due to a sampling of conservative sequences, an ancient, rapid radiation event or **taxon** sampling bias may also be contributing to the **ambiguity** problem. Results from analysis of a combined data set (organismal and molecular) are generally consistent with the inferences of the organismal character data regarding the colonial flagellates and are also consistent with the inferences of the sequence data regarding the unicellular taxa.

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=> index bioscience
FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                         ENTRY    SESSION
FULL ESTIMATED COST                                       5.88       6.10

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
       AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
       CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
       DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 09:40:10 ON 12 MAR 2009

68 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view
search error messages that display as 0* with SET DETAIL OFF.

=> s information and architecture and resolv? and (name or entity)
          1   FILE AQUASCI
         28   FILE BIOSIS
          5   FILE DISSABS
  27 FILES SEARCHED...
          1   FILE GENBANK
        342   FILE IFIPAT
          1   FILE MEDLINE
          1   FILE NTIS
          1   FILE OCEAN
         10   FILE PASCAL
          1   FILE PHIN
       2356   FILE PROMT
         15   FILE RDISCLOSURE
          9   FILE SCISEARCH
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      30386   FILE USPATFULL
          5   FILE USPATOLD
       5700   FILE USPAT2
          9   FILE WPIDS
          9   FILE WPINDEX

  18 FILES HAVE ONE OR MORE ANSWERS,   68 FILES SEARCHED IN STNINDEX

L5   QUE INFORMATION AND ARCHITECTURE AND RESOLV? AND (NAME OR ENTITY)

=> d rank
F1       30386   USPATFULL
F2        5700   USPAT2
F3        2356   PROMT
F4         342   IFIPAT
F5          28   BIOSIS
F6          15   RDISCLOSURE
F7          10   PASCAL
F8           9   SCISEARCH
F9           9   WPIDS
F10          9   WPINDEX
F11          5   DISSABS
F12          5   USPATOLD
F13          1   AQUASCI
F14          1   GENBANK
```

```
F15          1   MEDLINE
F16          1   NTIS
F17          1   OCEAN
F18          1   PHIN


=> file f5-f8 f11 f13-f18
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                         ENTRY    SESSION
FULL ESTIMATED COST                                       2.04       8.14

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=> s l5; dup rem l6
L6           73 L5


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PROCESSING COMPLETED FOR L6
L7           65 DUP REM L6 (8 DUPLICATES REMOVED)

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In a multifile environment, each file must have at least one valid
format requested.  Refer to file specific help messages or the
STNGUIDE file for information on formats available in individual
files.
REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):d bib 1-65
'D' IS NOT A VALID FORMAT
In a multifile environment, a format can only be used if it is valid
in at least one of the files.  Refer to file specific help messages
or the STNGUIDE file for information on formats available in
individual files.
REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):rnd
'RND' IS NOT A VALID FORMAT
In a multifile environment, a format can only be used if it is valid
in at least one of the files.  Refer to file specific help messages
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=> d bib 1-65
NO VALID FORMATS ENTERED FOR FILE 'GENBANK'
In a multifile environment, each file must have at least one valid
format requested. Refer to file specific help messages or the
STNGUIDE file for information on formats available in individual
files.
REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):d bib ab 1-60
'D' IS NOT A VALID FORMAT
In a multifile environment, a format can only be used if it is valid
in at least one of the files. Refer to file specific help messages
or the STNGUIDE file for information on formats available in
individual files.
REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):end

=> d bib ab 1-60

L7 ANSWER 1 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
Full Text
AN 2008:675023 BIOSIS
DN PREV200800675022
TI First investigation of the collagen D-band ultrastructure in fossilized
vertebrate integument.
AU Lingham-Soliar, Theagarten [Reprint Author]; Wesley-Smith, James
CS Univ KwaZulu Natal, EM Unit, ZA-4000 Durban, South Africa
linghamst@ukzn.ac.za
SO Proceedings of the Royal Society Biological Sciences Series B, (OCT 7
2008) Vol. 275, No. 1648, pp. 2207-2212.
ISSN: 0962-8452.
DT Article
LA English
ED Entered STN: 27 Nov 2008
Last Updated on STN: 27 Nov 2008
AB The ultrastructure of dermal fibres of a 200 Myr thunniform ichthyosaur,
Ichthyosaurus, specifically the 67 nm axial repeat D-banding of the
fibrils, which characterizes collagen, is presented for the first time by
means of scanning electron microscopy (SEM) analysis. The fragment of
material investigated is part of previously described fossilized skin
comprising an **architecture** of layers of oppositely oriented fibre
bundles. The wider implication, as indicated by the extraordinary quality
of preservation, is the robustness of the collagen molecule at the
ultrastructural level, which presumably contributed to its survival during
the initial processes of decomposition prior to mineralization.
Investigation of the elemental composition of the sample by SEM-energy
dispersive X-ray spectroscopy indicates that calcite and phosphate played
important roles in the rapid mineralization and fine replication of the
collagen fibres and fibrils. The exceedingly small sample used in the
investigation and high level of **information** achieved indicate the
potential for minimal damage to prized museum specimens; for example,
ultrastructural investigations by SEM may be used to help **resolve** highly
contentious questions, for example, 'protofeathers' in the Chinese
dinosaurs.

L7 ANSWER 2 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
Full Text
AN 2009:14937 BIOSIS
DN PREV200900014937
TI Anticipatory reward signals in ventral striatal neurons of behaving rats.
AU Khamassi, Mehdi; Mulder, Antonius B.; Tabuchi, Eiichi; Douchamps, Vincent;
Wiener, Sidney I. [Reprint Author]
CS Coll France, CNRS, Lab Physiol Percept and Act, 11 Pl Marcelin Berthelot,
F-75231 Paris 05, France
sidney.wiener@college-de-france.fr
SO European Journal of Neuroscience, (NOV 2008) Vol. 28, No. 9, pp.
1849-1866.
ISSN: 0953-816X.
DT Article
LA English
ED Entered STN: 17 Dec 2008

Last Updated on STN: 17 Dec 2008

AB It has been proposed that the striatum plays a crucial role in learning to select appropriate actions, optimizing rewards according to the principles of 'Actor-Critic' models of trial-and-error learning. The ventral striatum (VS), as Critic, would employ a temporal difference (TD) learning algorithm to predict rewards and drive dopaminergic neurons. This study examined this model's adequacy for VS responses to multiple rewards in rats. The respective arms of a plus-maze provided rewards of varying magnitudes; multiple rewards were provided at 1-s intervals while the rat stood still. Neurons discharged phasically prior to each reward, during both initial approach and immobile waiting, demonstrating that this signal is predictive and not simply motor-related. In different neurons, responses could be greater for early, middle or late droplets in the sequence. Strikingly, this activity often reappeared after the final reward, as if in anticipation of yet another. In contrast, previous TD learning models show decremental reward-prediction profiles during reward consumption due to a temporal-order signal introduced to reproduce accurate timing in dopaminergic reward-prediction error signals. To **resolve** this inconsistency in a biologically plausible manner, we adapted the TD learning model such that input **information** is nonhomogeneously distributed among different neurons. By suppressing reward temporal-order signals and varying richness of spatial and visual input **information**, the model reproduced the experimental data. This validates the feasibility of a TD-learning **architecture** where different groups of neurons participate in solving the task based on varied input **information**.

L7 ANSWER 3 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
Full Text

AN 2007:311509 BIOSIS

DN PREV200700313995

TI Separate conflict-specific cognitive control mechanisms in the human brain.

AU Egner, Tobias [Reprint Author]; Delano, Margaret; Hirsch, Joy

CS Northwestern Univ, Cognit Neurol and Alzheimers Dis Ctr, Feinberg Sch Med, 320 E Super,Searle 11, Chicago, IL 60611 USA
t-egner@northwestern.edu

SO NeuroImage, (APR 1 2007) Vol. 35, No. 2, pp. 940-948.
ISSN: 1053-8119.

DT Article

LA English

ED Entered STN: 16 May 2007
Last Updated on STN: 25 Jul 2007

AB To ensure optimal task performance, the human brain detects and **resolves** conflict in **information** processing via a cognitive control system. However, it is not known whether conflict resolution relies on a single central resource of cognitive control, or on a collection of independent control mechanisms that deal with different types of conflict. In order to. p address this question, we assessed behavioral and blood-oxygen-level-dependent (BOLD) responses during the simultaneous detection and resolution of two sources of conflict in a modified color-naming Stroop task: conflict stemming from incompatibility between the task-relevant and an irrelevant stimulus feature (stimulus-based or Stroop conflict), and conflict stemming from incompatibility between an irrelevant stimulus feature and response features (response-based or Simon conflict). Results show that control mechanisms recruited by stimulus-based conflict **resolve** stimulus-based conflict, but do not affect the resolution of response-based conflict, and vice versa. The resolution of response-based conflict was distinguished by modulation of activity in premotor cortex, whereas resolution of stimulus-based conflict was distinguished by the modulation of activity in parietal cortex. These results suggest that the human brain flexibly adopts, and independently controls, conflict-specific resolution strategies, biasing motor programming to **resolve** response-based conflict, and biasing stimulus representations to **resolve** stimulus-based conflict. We propose a non-centralized, modular **architecture** of cognitive control, where separate control resources operate in parallel, and are recruited in a context-sensitive manner. (c) 2006 Elsevier Inc. All rights reserved.

L7 ANSWER 4 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
Full Text

AN 2007:495836 BIOSIS

DN PREV200700497921
TI Can north american fish passage tools work for South american migratory fishes?.
AU Baigun, Claudio Rafael Mariano [Reprint Author]; Nestler, John Michael; Oldani, Norberto Oscar; Goodwin, R. Andrew; Weber, Larry J.
CS IIB INTECH, Camino Circunvalac Laguna,Km 6, RA-7120 Chascomus, Argentina claudiobaigun@intech.gov.ar; john.m.nestler@erdc.usace.army.mil; rag12@cornell.edu; gbio@ceride.gov.ar; larry-weber@uiowa.edu
SO Neotropical Ichthyology, (APR-JUN 2007) Vol. 5, No. 2, pp. 109-119. ISSN: 1679-6225.
DT Article
LA English
ED Entered STN: 20 Sep 2007
Last Updated on STN: 20 Sep 2007
AB In North America, the Numerical Fish Surrogate (NFS) is used to design fish bypass systems for emigrating j uveni le salmon as they migrate from hatchery outfalls and rearing habitats to adult habitat in the oceans. The NFS is constructed of three linked modules: 1) a computational fluid dynamics model describes the complex flow fields upstream of dams at a scale sufficiently **resolved** to analyze, understand and forecast fish movement, 2) a particle tracking model interpolates hydraulic **information** from the fixed nodes of the computational fluid model mesh to multiple locations relevant to migrating fish, and 3) a behavior model simulates the cognition and behavior of individual fish in response to the fluid dynamics predicted by the computational fluid dynamics model. These three modules together create a virtual reality where virtual fish exhibit realistic dam approach behaviors and can be counted at dam exits in ways similar to the real world. Once calibrated and validated with measured fish movement and passage data, the NFS can accurately predict fish passage proportions with sufficient precision to allow engineers to select one optimum alternative from among many competing structural or operational bypass alternatives. Although South American fish species are different from North American species, it is likely that the basic computational **architecture** and numerical methods of the NFS can be used for fish conservation in South America. Consequently, the extensive investment made in the creation of the NFS need not be duplicated in South America. However, its use in South America will require that the behavioral response of the continent's unique fishes to hydrodynamic cues must be described, codified and tested before the NFS can be used to conserve fishes by helping design efficient South American bypass systems. To this end, we identify studies that could be used to describe the movement behavior of South American fishes of sufficient detail that they could be used to develop, calibrate and validate a South American version of the NFS.

L7 ANSWER 5 OF 65 DISSABS COPYRIGHT (C) 2009 ProQuest Information Full Text and Learning Company; All Rights Reserved on STN
AN 2008:66239 DISSABS Order Number: AAI3310986
TI Integrating business rules of **information** systems with enterprise **architecture**
AU Van, Jung Woo [D.Mgt.]; Steenkamp, Annette L. [advisor]
CS Lawrence Technological University (0332)
SO Dissertation Abstracts International, (2006) Vol. 69, No. 5A, p. 1882. Order No.: AAI3310986. 267 pages.
ISBN: 978-0-549-60361-0.
DT Dissertation
FS DAI
LA English
ED Entered STN: 20081205
Last Updated on STN: 20081205
AB < Pub Inc> Due to the inherent complexity of enterprise integration, business rules embedded within the heterogeneous and acquired **information** systems are often not aligned with the business policies defined in the enterprise strategy. Despite recent research efforts on business rule integration within the scope of enterprise **architecture**, most research has focused on top-down enterprise strategies of business rule integration, but research on business rule integration of **information** systems with the enterprise **architecture** are lacking. This dissertation examines a systematic approach to **resolving** the business rule integration issues within the enterprise from the perspective of **information** system business rule integration. In this research

conceptual models for business rule integration are developed. A Business Rule Integration Meta-model Framework (BRIMF), which describes the relationships and associations of the key enterprise **entities** forming the baseline **architecture** for the business rule integration solution, is proposed. A Business Rule Alignment Process Model (BRAPM) and a Business Rule Alignment Methodology (BRAM) are proposed as a formalized approach to align the business rules embedded in **information** systems with the business rules defined in the enterprise **architecture**. A Business Rule Mapping Model (BRMM), which represents one of the stages within the BRAPM, is presented to demonstrate the business rule mapping algorithm as well as identified mapping discrepancy cases. A key benefit of the BRIMF, BRAPM, BRAM and BRMM is the ability to align business rules, extracted from **information** systems, with the business rules defined at the enterprise **architecture** level by using the Business Rule Language Plus (BRL+) for data storage in the enterprise repository. As a constructive validation of the application of the conceptual models a hybrid approach, which adopts mixed techniques to case design and prototyping is employed to demonstrate the effectiveness of the concepts.

L7 ANSWER 6 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN Full Text
AN 2007:245879 BIOSIS
DN PREV200700250177
TI Advances in Photosynthesis and Respiration:THE LIGHT-DRIVEN PLASTOCYANIN: FERREDOXIN OXIDOREDUCTASE.
AU Golbeck, JH [Editor]
SO Golbeck, JH [Editor]. (2006) Advances in Photosynthesis and Respiration:THE LIGHT-DRIVEN PLASTOCYANIN: FERREDOXIN OXIDOREDUCTASE. Publisher: SPRINGER, PO BOX 17, 3300 AA DORDRECHT, NETHERLANDS. Series: ADVANCES IN PHOTOSYNTHESIS AND RESPIRATION. ISBN: 978-1-4020-4255-3(H).
DT Book
LA English
ED Entered STN: 18 Apr 2007
Last Updated on STN: 18 Apr 2007
AB This 716-page book is volume 24 in the series ''Advances in Photosynthesis and Respiration'', and this volume summarizes the advances made in the last decade in the biophysics, biochemistry, and molecular biology of the light-driven plastocyanin:ferrodoxin oxidoreductase, known as Photosystem I. This reaction center participates with Photosystem II in harvesting solar energy to supply photosynthetic organisms with stored chemical energy in the form of ATP and stored reducing power in the form of NADPH for processes such as metabolism, growth, and reproduction. This volume contains 40 individually-authored chapters divided among 11 thematic parts. Part I of the book focuses on historical perspectives, and part II concentrates on the molecular **architecture** of Photosystem I. Parts III-VIII discuss, respectively, pigment-protein interactions, excitation dynamics and electron transfer processes, modification of the cofactors and their environments, spectroscopic studies of the cofactors, kinetics of electron transfer, and biosynthetic processes. Topics covered in the remaining 3 parts of the book include modeling of photosynthetic processes, related processes, and evolution of Photosystem I. The book is indexed by subject, organism, mutant, and gene and gene product. The book also includes an author index, and a color plate section. The text is written in English. This book is intended to be a comprehensive and up-to-date source of background **information** on Photosystem I for seasoned researchers, those who are just entering the field, Ph.D. students, researchers and advanced undergraduates in the fields of biophysics, biochemistry, microbiology, agriculture, and ecology. Industrial scientists, interested in solar energy conversion, will also find the book useful.

L7 ANSWER 7 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN Full Text
AN 2007:503835 BIOSIS
DN PREV200700507217
TI Theoretical scenarios for research and development needs to save dwindling sturgeon populations in the Caspian Sea.
AU Mathews, C. P.; Peacock, N.; Gilkolei, R.
CS christopherpmathews@yahoo.co.uk
SO Journal of Applied Ichthyology, (DEC 2006) Vol. 22, No. Suppl. 1, pp. 132-139.

CODEN: JAICEF. ISSN: 0175-8659.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 26 Sep 2007
Last Updated on STN: 26 Sep 2007
AB Current landings of Caspian sturgeon fell from a peak of about 30,000 tonnes in 1977 to about 1,000 tonnes in 2002. Maximum Sustainable Yield (MSY) of Caspian sturgeon is unknown but may be in the range of about 22,500 t/yr. Total Allowable Catches (TACs) fell from about 15,000 t/yr in 1992 to = 500 t/yr in 20022004. It is widely believed that Illegal Unreported and Unregulated (IUU) sturgeon fishing accounts for 90% of real sturgeon landings, but estimates of IUU landings were not included in any TAC assessments. FAO (2004) reported that assessments were not transparent. Rough estimates of stock recovery based on 2002-04 landings and a doubling time of about 14 years suggest that, even in the unlikely event of a total moratorium on legal and (IUU) fishing for about 50 years, stocks could only provide sustainable landings of 4,000 to 8,000 t/yr. Clearly, total recruitment was insufficient to support total effort expended by legal and IUU fishing. In November 1995, after several years of preliminary work and regional consultations, CITES established a ban on international trade in Caspian sturgeon products.Accurate biological data on sturgeon exist in most ex-Soviet countries, but cannot be accessed. Available data on mortality and recruitment do not support dynamic pool, VPA, yield per recruit or stock/recruitment models; catch and effort data are available from Iranian waters from 1990, but can presently not support surplus production modelling of important Caspian wide stocks. It is therefore impossible to apply any of the usual assessment methods to Caspian sturgeon stocks. Nevertheless it is clear that these are depleted, face extinction, and require proactive management starting in the immediate future if they are to be conserved. Accessible data and "guesstimates" have been used in an attempt to identify new scenarios and to inform management. A simple bio-economic model based on available **information** and "guesstimates" about key parameters was used to estimate Recovery Rates (RR, %MSY/year) needed to provide Internal Rates of Return (IRR) of 5%-20%. RRs of around 1.0-2.0% MSY/year are needed to support commercially bankable IRRs of = 10% over 25-50 years. The model suggests that a private sector investment of about _ 500,000,000 in restocking, repayable over 50 years, may be feasible. Resulting benefits of such an investment would include from around US 500$ 1.0 Billion/year for the foreseeable future. Private sector funding will become available only when a transparent and well structured institutional **architecture** is provided for Coastal Zone Management (CZM) of the fishery, so that IUU fishing can be controlled. Issues not addressed by the model that must also be **resolved** include rehabilitation of spawning and nursery grounds, pollution control, careful control of genetic problems associated with restocking, access to sufficient brood stock and full implementation of the Caspian Framework Convention and all of its protocols. Challenges and limitations of such a project are discussed.

L7 ANSWER 8 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
Full Text
AN 2006:341336 BIOSIS
DN PREV200600348554
TI **Resolving** fiber crossing using advanced fast marching tractography based on diffusion tensor imaging.
AU Staempfli, P.; Jaermann, T.; Crelier, G. R.; Kollias, S.; Valavanis, A.; Boesiger, P. [Reprint Author]
CS ETH, Inst Biomed Engn, Gloriastr 35, CH-8092 Zurich, Switzerland
staempfli@biomed.ee.ethz.ch; boesiger@biomed.ee.ethz.ch
SO NeuroImage, (MAR 2006) Vol. 30, No. 1, pp. 110-120.
ISSN: 1053-8119.
DT Article
LA English
ED Entered STN: 12 Jul 2006
Last Updated on STN: 12 Jul 2006
AB Magnetic resonance diffusion tensor tractography is a powerful tool for the non-invasive depiction of the white matter **architecture** in the human brain. However, due to limitations in the underlying tensor model, the technique is often unable to reconstruct correct trajectories in heterogeneous fiber arrangements, such as axonal crossings. A novel tractography method based on fast marching (FM) is proposed which is

capable of **resolving** fiber crossings and also permits trajectories to branch. It detects heterogeneous fiber arrangements by incorporating **information** from the entire diffusion tensor. The FM speed function is adapted to the local tensor characteristics, allowing in particular to maintain the front evolution direction in crossing situations. In addition, the FM's discretization error is reduced by increasing the number of considered possible front evolution directions. The performance of the technique is demonstrated in artificial data and in the healthy human brain. Comparisons with standard FM tractography and conventional line propagation algorithms show that, in the presence of interfering structures, the proposed method is more accurate in reconstructing trajectories. The in vivo results illustrate that the elucidated major white matter pathways are consistent with known anatomy and that multiple crossings and tract branching are handled correctly. (c) 2005 Elsevier Inc. All rights reserved.

L7 ANSWER 9 OF 65 DISSABS COPYRIGHT (C) 2009 ProQuest Information
Full Text
and Learning Company; All Rights Reserved on STN
AN 2006:33037 DISSABS Order Number: AAI3191693
TI Search and retrieval algorithms for distributed data management systems
AU Zeinalipour-Yazti, Demetrios [Ph.D.]; Gunopulos, Dimitrios [advisor]; Kalogeraki, Vana [advisor]
CS University of California, Riverside (0032)
SO Dissertation Abstracts International, (2005) Vol. 66, No. 10B, p. 5517. Order No.: AAI3191693. 155 pages.
ISBN: 0-542-34682-6.
DT Dissertation
FS DAI
LA English
ED Entered STN: 20060621
Last Updated on STN: 20060621
AB Modern Data Management Systems have to cope with data that is generated automatically and continuously across distributed and potentially geographically diverse locations. Organizing **information** in centralized repositories is becoming increasingly expensive and in many occasions impractical.

This dissertation introduces novel search and retrieval algorithms for Distributed Data Management Systems. In our setting, the **information** remains in-situ until users request to retrieve it. Our objective is to minimize the utilization of the communication medium and to exploit the inherent parallelism of a distributed environment. Additionally, I consider the challenges of a graph topology between distributed nodes, which is ubiquitous in emerging fields such as Peer-to-Peer Networks, Sensor Networks and Vehicular Networks.

Specifically, this dissertation makes the following contributions: (1) Threshold Join Algorithm (TJA), which is a distributed top-K query processing algorithm that operates over a set of exact scores. TJA uses a non-uniform threshold on the queried attribute in order to minimize the number of data objects that have to be transferred towards the querying node. Additionally, TJA **resolves** queries in the network rather than in a centralized fashion, which minimizes even more the consumption of bandwidth and delay. (2) LB-K and UBLB-K Algorithms , which are specialized distributed top-K query processing algorithms that operate over distributed lower and upper bounds in order to minimize the number of data objects transferred towards the querying engine. (3) Intelligent Search Mechanism (ISM), which is an efficient and scalable technique to route query messages in unstructured Peer-to-Peer systems. ISM is efficient because its performance is bounded by the number of neighbors and scalable because no global knowledge is required to be maintained. ISM also serves as the query routing component in our open source Peerware **architecture**. (4) Distributed Domain **Name** Order Algorithm (DDNO), which alleviates the burden incurred by the topology mismatch between the underlying physical network and the overlay network of Peer-to-Peer systems, by clustering topologically close-by nodes together.

My dissertation shows that traditional search and retrieval methods can be improved by an order of magnitude by using a combination of local query processing techniques, in-network aggregation and awareness of the underlying network topology.

L7 ANSWER 10 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
Full Text

STN
AN 2005:309453 BIOSIS
DN PREV200510096386
TI Structural insights into a yeast prion illuminate nucleation and strain diversity.
AU Krishnan, Rajaraman; Lindquist, Susan L. [Reprint Author]
CS Whitehead Inst Biomed Res, 9 Cambridge Ctr, Cambridge, MA 02142 USA
Lindquist_admin@wi.mit.edu
SO Nature (London), (JUN 9 2005) Vol. 435, No. 7043, pp. 765-772.
CODEN: NATUAS. ISSN: 0028-0836.
DT Article
LA English
ED Entered STN: 15 Aug 2005
Last Updated on STN: 26 Sep 2007
AB Self-perpetuating changes in the conformations of amyloidogenic proteins play vital roles in normal biology and disease. Despite intense research, the **architecture** and conformational conversion of amyloids remain poorly understood. Amyloid conformers of Sup35 are the molecular embodiment of the yeast prion known as [PSI], which produces heritable changes in phenotype through self-perpetuating changes in protein folding. Here we determine the nature of Sup35' s cooperatively folded amyloid core, and use this **information** to investigate central questions in prion biology. Specific segments of the amyloid core form intermolecular contacts in a 'Head-to-Head', 'Tail-to-Tail' fashion, but the 'Central Core' is sequestered through intramolecular contacts. The Head acquires productive interactions first, and these nucleate assembly. Variations in the length of the amyloid core and the nature of intermolecular interfaces form the structural basis of distinct prion 'strains', which produce variant phenotypes in vivo. These findings **resolve** several problems in yeast prion biology and have broad implications for other amyloids.

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Full Text
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AN 2005-0149318 PASCAL
CP Copyright © 2005 INIST-CNRS. All rights reserved.
TIEN Algorithm for DNSSEC trusted key rollover
ICOIN 2005 : **information** networking : convergence in broadband and mobile networking : Jeju Island, 31 January - 2 February 2005
AU GUETTE Gilles; COUSIN Bernard; FORT David
KIM Cheeha (ed.)
CS IRISA, Campus de Beaulieu, 35042 Rennes, France
SO Lecture notes in computer science, (2005), 3391, 679-688, 14 refs.
Conference: International conference on information networking, (Korea, Republic of), 31 Jan 2005
ISSN: 0302-9743
ISBN: 3-540-24467-0
DT Journal; Conference
BL Analytic
CY Germany, Federal Republic of
LA English
AV INIST-16343, 354000124442130710
AB The Domain **Name** System Security Extensions (DNSSEC) **architecture** is based on public-key cryptography. A secure DNS zone has one or more keys and signs its resource records with these keys in order to provide two security services: data integrity and authentication. These services allow to protect DNS transactions and permit the detection of attempted attacks on DNS. The DNSSEC validation process is based on the establishment of a chain of trust between zones. This chain needs a secure entry point: a DNS zone whose at least one key is trusted. In this paper we study a critical problem associated to the key rollover in DNSSEC: the trusted keys rollover problem. We propose an algorithm that allows a **resolver** to update its trusted keys automatically and in a secure way without any delay or any break of the DNS service.

L7 ANSWER 12 OF 65 PASCAL COPYRIGHT 2009 INIST-CNRS. ALL RIGHTS
Full Text
RESERVED. on STN DUPLICATE 1
AN 2006-0090448 PASCAL
CP Copyright © 2006 INIST-CNRS. All rights reserved.
TIEN On the controlled evolution of access rules in cooperative **information** systems

On the move to meaningful internet systems 2005 : CoopIS, DOA, and ODBASE : OTM Confederated International Conferences, CoopIS, DOA, and ODBASE 2005, Agia Napa, Cyprus, October 31- November 4, 2005 : proceedings
AU RINDERLE Stefanie; REICHERT Manfred
CS Department Databases and Information Systems, University of Ulm, Germany, Federal Republic of; Information Systems Group, University of Twente, Netherlands
SO Lecture notes in computer science, (2005), 3760, 238-255, 29 refs.
Conference: OTM Confederated International Conferences, Agia Napa (Cyprus), 31 Oct 2005
ISSN: 0302-9743
ISBN: 3-540-29736-7
DT Journal; Conference
BL Analytic
CY Germany, Federal Republic of
LA English
AV INIST-16343, 354000138666870140
AB For several reasons enterprises are frequently subject to organizational change. Respective adaptations may concern business processes, but also other components of an enterprise **architecture**. In particular, changes of organizational structures often become necessary. The **information** about organizational **entities** and their relationships is maintained in organizational models. Therefore the quick and correct adaptation of these models is fundamental to adequately cope with changes. However, model changes alone are not sufficient to guarantee consistency. Since organizational models also provide the basis for defining access rules (e.g., actor assignments in workflow management systems or access rules in document-centered applications) this **information** has to be adapted accordingly (e.g., to avoid non-**resolvable** actor assignments). Current approaches do not adequately address this problem, which often leads to security gaps and delayed change adaptations. In this paper we present a comprehensive approach for the controlled evolution of organizational models in cooperative **information** systems. First, we introduce a set of operators with well-defined semantics for defining and changing organizational models. Second, we present an advanced approach for the semi-automated adaptation of access rules when the underlying organizational model is changed. This includes a formal part concerning both the evolution of organizational models and the adaptation of related access rules.

L7 ANSWER 13 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on Full Text
STN
AN 2005:383112 BIOSIS
DN PREV200510159424
TI Does consciousness really collapse the wave function? - A possible objective biophysical resolution of the measurement problem.
AU Thaheld, Fred H. [Reprint Author]
CS 99 Cable Circle 20, Folsom, CA 95630 USA
fthaheld@directcon.net
SO Biosystems, (AUG 2005) Vol. 81, No. 2, pp. 113-124.
CODEN: BSYMBO. ISSN: 0303-2647.
DT Article
LA English
ED Entered STN: 21 Sep 2005
Last Updated on STN: 21 Sep 2005
AB An analysis has been performed of the theories and postulates advanced by von Neumann, London and Bauer, and Wigner, concerning the role that consciousness might play in the collapse of the wave function, which has become known as the measurement problem. This reveals that an error may have been made by them in the area of biology and its interface with quantum mechanics when they called for the reduction of any superposition states in the brain through the mind or consciousness. Many years later Wigner changed his mind to reflect a simpler and more realistic objective position which appears to offer a way to **resolve** this issue. The argument is therefore made that the wave function of any superposed photon state or states is always objectively and stochastically changed within the complex **architecture** of the eye in a continuous linear process initially for most of the superposed photons, followed by a discontinuous nonlinear collapse process later for any remaining superposed photons, thereby guaranteeing that only final, measured **information** is presented to the brain, mind or consciousness. An experiment to be conducted in the

near future may enable us to simultaneously **resolve** the measurement problem and also determine if the linear nature of quantum mechanics is violated by the perceptual process. (c) 2005 Elsevier Ireland Ltd. All rights reserved.

L7 ANSWER 14 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on Full Text
STN
AN 2005:380664 BIOSIS
DN PREV200510159031
TI Watching the components of photosynthetic bacterial membranes and their in situ organisation by atomic force microscopy.
AU Scheuring, Simon; Levy, Daniel; Rigaud, Jean-Louis [Reprint Author]
CS CNRS, Inst Curie, UMR 168, 11 Rue Pierre and Marie Curie, F-75231 Paris 05, France
rigaud@curie.fr
SO Biochimica et Biophysica Acta, (JUN 30 2005) Vol. 1712, No. 2, pp. 109-127.
ISSN: 0005-2736.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 21 Sep 2005
Last Updated on STN: 21 Sep 2005
AB The atomic force microscope has developed into a powerful tool in structural biology allowing **information** to be acquired at submolecular resolution on the protruding Structures of membrane proteins. It is now a complementary technique to X-ray crystallography and electron microscopy for structure determination of individual membrane proteins after extraction, purification and reconstitution into lipid bilayers. Moving on from the structures of individual components of biological membranes, atomic force microscopy has recently been demonstrated to be a unique tool to identify in situ the individual components of multi-protein assemblies and to study the supramolecular **architecture** of these components allowing the efficient performance of a complex biological function.Here, recent atomic force microscopy studies of native membranes of different photosynthetic bacteria with different polypeptide contents are reviewed. Technology, advantages, feasibilities, restrictions and limits of atomic force microscopy for the acquisition of highly **resolved** images of up to 10 angstrom lateral resolution under native conditions are discussed. From a biological point of view, the new insights contributed by the images are analysed and discussed in the context of the strongly debated organisation of the interconnected network of membrane-associated chlorophyll-protein complexes composing the photosynthetic apparatus in different species of purple bacteria. (c) 2005 Elsevier B.V. All rights reserved.

L7 ANSWER 15 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on Full Text
STN
AN 2006:207458 BIOSIS
DN PREV200600209186
TI Coherence backscattering spectroscopy (cbs): a novel modality for colorectal cancer (CRC) risk stratification.
AU Roy, Hemant; Kim, Young; Wali, Ramesh; Liu, Yang; Koetsier, Jennifer; Kunte, Dhananjay; Goldberg, Michael J.; Backman, Vadim
SO Gastroenterology, (APR 2005) Vol. 128, No. 4, Suppl. 2, pp. A28.
Meeting Info.: Annual Meeting of the American-Gastroenterological-Association/Digestive-Disease-Week. Chicago, IL, USA. May 14 -19, 2005. Amer Gastroenterol Assoc.
CODEN: GASTAB. ISSN: 0016-5085.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 29 Mar 2006
Last Updated on STN: 29 Mar 2006
AB Members of our group have been involved in pioneering light-scattering technologies for diagnosis of dysplasia (Nature 2000, Nature Med 2001). Here we report that a novel depth-**resolved** light scattering technique, CBS, enables detection of the micro-architectural changes of the "field effect" and thus may be utilized for CRC risk-stratification. Coherence backscattering is a phenomenon caused by constructive interference of

light waves traveling timereversed paths and encodes **information** about tissue nano/micro-**architecture**. We have recently overcome the technical obstacles that have prevented previous CBS analysis of (issue, thus providing a means to obtain unparalleled depth-selective ultrastructural **information**. (Optics Letters 2004, Applied Optics 2005). We, therefore, tested the ability of CBS to determine CRC risk.Methods: In order to demonstrate that CBS markers develop early in colon carcinogenesis, we evaluated preneoplastic time-points in the azoxymethane (AOM)-treated rat and MIN mouse models of CRC and compared with age-matched controls. Furthermore, we performed a pilot human trial using 37 patients undergoing screening colonoscopy comparing CBS markers obtained from endoscopically normal mucosa from patients with and without adenomas. CBS analysis was conducted on fresh colonic mucosal biopsies using a CBS apparatus.Results:[GRAPHICS]We analyzed two previously validated spectral markers: spectral slope S.S and the score of first two principal components (PC) obtained from the principal component analysis (Gastroenterology 2004). These parameters were dramatically altered early in neoplasia in models and their relevance in humans was confirmed (see table). Conclusions We demonstrate, for the first time, that CBS analysis of the histologically normal mucosa resulted in unprecedented accuracy in detecting the "field effect". Thus, CBS has considerable promise for tailoring CRC screening strategies based on risk.

L7 ANSWER 16 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
Full Text
STN
AN 2005:154031 BIOSIS
DN PREV200500153118
TI Translational neurochemical research in acute human brain injury: The current status and potential future for cerebral microdialysis.
AU Hillered, Lars [Reprint Author]; Vespa, Paul M.; Hovda, David A.
CS Dept NeurosciDiv Neurosurg, Univ Uppsala Hosp, SE-75185, Uppsala, Sweden lars.hillered@neurokir.uu.se
SO Journal of Neurotrauma, (January 2005) Vol. 22, No. 1, pp. 3-41. print. ISSN: 0897-7151 (ISSN print).
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 20 Apr 2005
Last Updated on STN: 20 Apr 2005
AB Microdialysis (MD) was introduced as an intracerebral sampling method for clinical neurosurgery by Hillered et al. and Meyerson et al. in 1990. Since then MD has been embraced as a research tool to measure the neurochemistry of acute human brain injury and epilepsy. In general investigators have focused their attention to relative chemical changes during neurointensive care, operative procedures, and epileptic seizure activity. This initial excitement surrounding this technology has subsided over the years due to concerns about the amount of tissue sampled and the complicated issues related to quantification. The interpretation of mild to moderate MD fluctuations in general remains an issue relating to dynamic changes of the **architecture** and size of the interstitial space, blood-brain barrier (BBB) function, and analytical imprecision, calling for additional validation studies and new methods to control for in vivo recovery variations. Consequently, the use of this methodology to influence clinical decisions regarding the care of patients has been restricted to a few institutions. Clinical studies have provided ample evidence that intracerebral MD monitoring is useful for the detection of overt adverse neurochemical conditions involving hypoxia/ischemia and seizure activity in subarachnoid hemorrhage (SAH), traumatic brain injury TBI), thromboembolic stroke, and epilepsy. There is some data strongly suggesting that MD changes precede the onset of secondary neurological deterioration following SAH, hemispheric stroke, and surges of increased ICP in fulminant hepatic failure. These promising investigations have relied on MD-markers for disturbed glucose metabolism (glucose, lactate, and pyruvate) and amino acids. Others have focused on trying to capture other important neurochemical events, such as excitotoxicity, cell membrane degradation, reactive oxygen species (ROS) and nitric oxide (NO) formation, cellular edema, and BBB dysfunction. However, these other applications need additional validation. Although these cerebral events and their corresponding changes in neurochemistry are important, other promising MD applications, as yet less explored, comprise local neurochemical provocations, drug penetration to the human brain, MD as a

tool in clinical drug trials, and for studying the proteomics of acute human brain injury. Nevertheless, MD has provided new important insights into the neurochemistry of acute human brain injury. It remains one of very few methods for neurochemical measurements in the interstitial compartment of the human brain and will continue to be a valuable translational research tool for the future. Therefore, this technology has the potential of becoming an established part of multimodality neuro-ICU monitoring, contributing unique **information** about the acute brain injury process. However, in order to reach this stage, several issues related to quantification and bedside presentation of MD data, implantation strategies, and quality assurance need to be **resolved.** The future success of MD as a diagnostic tool in clinical neurosurgery depends heavily on the choice of biomarkers, their sensitivity, specificity, and predictive value for secondary neurochemical events, and the availability of practical bedside methods for chemical analysis of the individual markers. The purpose of this review was to summarize the results of clinical studies using cerebral MD in neurosurgical patients and to discuss the current status of MD as a potential method for use in clinical decision-making. The approach was to focus on adverse neurochemical conditions in the injured human brain and the MD biomarkers used to study those events. Methodological issues that appeared critical for the future success of MD as a routine intracerebral sampling method were addressed.

L7 ANSWER 17 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on Full Text
STN
AN 2004:462014 BIOSIS
DN PREV200400464368
TI AdoMet radical proteins - from structure to evolution - alignment of divergent protein sequences reveals strong secondary structure element conservation.
AU Nicolet, Yvain; Drennan, Catherine L. [Reprint Author]
CS Dept Chem 16 573, MIT, 77 Massachusetts Ave, Cambridge, MA, 02139, USA cdrennan@mit.edu
SO Nucleic Acids Research, (2004) Vol. 32, No. 13, pp. 4015-4025. print. ISSN: 0305-1048 (ISSN print).
DT Article
LA English
ED Entered STN: 1 Dec 2004
Last Updated on STN: 1 Dec 2004
AB Eighteen subclasses of S-adenosyl-L-methionine (AdoMet) radical proteins have been aligned in the first bioinformatics study of the AdoMet radical superfamily to utilize crystallographic **information.** The recently **resolved** X-ray structure of biotin synthase (BioB) was used to guide the multiple sequence alignment, and the recently **resolved** X-ray structure of coproporphyrinogen III oxidase (HemN) was used as the control. Despite the low 9% sequence identity between BioB and HemN, the multiple sequence alignment correctly predicted all but one of the core helices in HemN, and correctly predicted the residues in the enzyme active site. This alignment further suggests that the AdoMet radical proteins may have evolved from half-barrel structures (alphabeta)4 to three-quarter-barrel structures ((06 to full-barrel structures (alphabeta)8. It predicts that anaerobic ribonucleotide reductase (RNR) activase, an ancient enzyme that, it has been suggested, serves as a link between the RNA and DNA worlds, will have a half-barrel structure, whereas the three-quarter barrel, exemplified by HemN, will be the most common **architecture** for AdoMet radical enzymes, and fewer members of the superfamily will join BioB in using a complete (alphabeta)8 TIM-barrel fold to perform radical chemistry. These differences in barrel **architecture** also explain how AdoMet radical enzymes can act on substrates that range in size from 10 atoms to 608 residue proteins.

L7 ANSWER 18 OF 65 PASCAL COPYRIGHT 2009 INIST-CNRS. ALL RIGHTS Full Text
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AN 2005-0062200 PASCAL
CP Copyright © 2005 INIST-CNRS. All rights reserved.
TIEN The roles of ontology and metadata registry for interoperable databases
Distributed computing and internet technology : Bhubaneswar, 22-24 December 2004
AU LEE Jeong-Oog; KO Myeong-Cheol; PAIK Woojin; HEUNG SEOK JEON; KIM Junghwan; KANG Hyun-Kyu; KIM Jinsoo

GHOSH R.K. (ed.); MOHANTY Hrushikesha (ed.)
CS Dept. of Computer Science, Konkuk University, 322 Danwol-dong, Chungju-si, Chungcheongbuk-do, 380-701, Korea, Republic of
SO Lecture notes in computer science, (2004), 3347, 217-226, 16 refs. Conference: 1 ICDCIT 2004 ; international conference on distributed computing and internet technology, Bhubaneswar (India), 22 Dec 2004 ISSN: 0302-9743 ISBN: 3-540-24075-6
DT Journal; Conference
BL Analytic
CY Germany, Federal Republic of
LA English
AV INIST-16343, 354000124400700220
AB In order to make multiple autonomous databases to interoperate effectively, semantic heterogeneities have to be detected and **resolved**. Another difficulty is that users can be allowed to handle **information** easily from different heterogeneous databases that refer to the same real-world **entity**. To solve these problems, in this paper, I present an **information** integration system for interoperable databases using metadata registry and ontology. A metadata registry is a place to keep facts about characteristics of data that are necessary for data sharing and exchange in a specific domain. An ontology defines concepts and relations among concepts. The purpose of the proposed **architecture** is to define an **information** integration model, which combines characteristics of both standard specification of metadata registry and functionality of ontology for the concepts and relations.

L7 ANSWER 19 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on Full Text
STN
AN 2005:13183 BIOSIS
DN PREV200500019073
TI Solution structure of the Tn3 **resolvase**-crossover site synaptic complex.
AU Nollmann, Marcelo; He, Jiuya; Byron, Olwyn; Stark, W. Marshall [Reprint Author]
CS Inst BIomed and Life SciDiv Mol Genet, Univ Glasgow, Glasgow, Lanark, G11 6NU, UK
m.stark@bio.gla.ac.uk
SO Molecular Cell, (October 8 2004) Vol. 16, No. 1, pp. 127-137. print. ISSN: 1097-2765 (ISSN print).
DT Article
LA English
ED Entered STN: 22 Dec 2004
Last Updated on STN: 22 Dec 2004
AB Tn3 **resolvase** is a site-specific DNA recombinase, which catalyzes strand exchange in a synaptic complex containing twelve **resolvase** subunits and two res sites. Hyperactive mutants of **resolvase** can form a simpler complex (X synapse) containing a **resolvase** tetramer and two shorter DNA segments at which strand exchange takes place (site 1). We have solved the low-resolution solution structure of the purified catalytically competent X synapse from small-angle neutron and X-ray scattering data, using methods in which the data are fitted with models constructed by rigid body transformations of a published crystallographic structure of a **resolvase** dimer bound to site I. Our analysis reveals that the two site I fragments are on the outside of a **resolvase** tetramer core and provides some **information** on the quaternary structure of the tetramer. We discuss implications of our structure for the **architecture** of the natural synaptic complex and the mechanism of strand exchange.

L7 ANSWER 20 OF 65 DISSABS COPYRIGHT (C) 2009 ProQuest Information Full Text
and Learning Company; All Rights Reserved on STN
AN 2004:46732 DISSABS Order Number: AAI3114885
TI Discrete-event simulations for control and analysis of distributed systems
AU Ramakrishnan, Sreeram [Ph.D.]; Wysk, Richard A. [advisor]
CS The Pennsylvania State University (0176)
SO Dissertation Abstracts International, (2003) Vol. 64, No. 12B, p. 6271. Order No.: AAI3114885. 175 pages.
DT Dissertation
FS DAI
LA English
ED Entered STN: 20040902

Last Updated on STN: 20040902

AB The concept of simulation-based control has been well-established for discrete-part manufacturing domain. However, issues related to extending that **architecture** to control distributed **entities** have not been **resolved**. As the amount of detail that need to be modeled in a simulation that will be used as a control execution mechanism grows, it necessitates adopting various decomposition methods such as distributed modeling. The main challenge associated with distributed modeling is the synchronization of their clocks and maintaining causality of their interactions. Several simulation-based integration **architectures** that allow for the real time control and/or fast global analysis of distributed systems exist. However, no **architecture** provides a coordination mechanism or an integration framework for distributed simulations that can be used both for real time control and for fast analysis without the need of any rollback mechanisms and allowing the interaction with multipass models that can be used for localized fast analysis.

This thesis primarily focuses on developing a generic, object-oriented modeling methodology and integration framework, Distributed Simulations for Analysis and Control (DISIAC), that enables a set of distributed simulation models, fit within a common **architecture**, to serve as a control execution mechanism and as a tool for global fast analysis. The individual federates have access to multipass models for that **entity** which can serve as a localized fast analysis tool and/or as a decision-making tool. This framework integrates the simulation models with the control execution system, databases with product and production schedule **information**, and simulation models of other **entities** in the distributed system. The **architecture** enables the federation to interact with external optimization tools to respond to any changes in their operating condition.

A Federation Simulation Coordinator (FSC) that coordinates the functioning of the simulation models in both modes is presented along with a variation of exact synchronization mechanism developed in this research. A case study based on a real-life example of a Printed Circuit Board (PCB) assembly supply chain segment is used to illustrate the functioning and the utility of the modeling approach presented in this thesis, and discuss various factors that affect the performance of a system modeled using DISIAC.

L7 ANSWER 21 OF 65 PHIN COPYRIGHT 2009 Informa UK Ltd on STN
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AN 2003:4585 PHIN
DED 12 Feb 2003
TI Faster access to life-saving drugs: how EU legislation might speed up the assessment of drugs that promise significant public health benefits
SO Scrip (2003) No. 2823 Review Issue 2002 p14
DT Newsletter
FS FULL

L7 ANSWER 22 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
Full Text
STN
AN 2004:76224 BIOSIS
DN PREV200400078288
TI Neural mechanisms of cortico-cortical interaction in texture boundary detection: A modeling approach.
AU Thielscher, A. [Reprint Author]; Neumann, H.
CS Department of Psychiatry, University of Ulm, Leimgrubenweg 12-14, 89075, Ulm, Germany
axel.thielscher@medizin.uni-ulm.de
SO Neuroscience, (15 December 2003) Vol. 122, No. 4, pp. 921-939. print.
CODEN: NRSCDN. ISSN: 0306-4522.
DT Article
LA English
ED Entered STN: 4 Feb 2004
Last Updated on STN: 4 Feb 2004

AB Texture **information** is an elementary feature utilized by the human visual system to automatically, or preattentively, segment the visual scene. The neural substrate underlying human texture processing as well as the basic computational mechanisms remains largely unknown up to now. We propose a neural model of texture processing which integrates the data obtained by a variety of methods into a common computational framework.

It consists of a hierarchy of bi-directionally linked visual areas each containing topographical maps of mutually interconnected cells. It builds upon the two key hypotheses that (i) texture segmentation is based on boundary detection and that (ii) texture border detection is mainly a function of higher visual cortical areas such as V4. This model, while attempting to explain the processing of textures, is embedded in a more general neural model **architecture** of the infero-temporal pathway of form processing. The model allows to link human performance in texture segmentation with model cell activation patterns, in turn permitting to trace back fundamental psychophysical results on texture processing to their putative neural origins. Most importantly, it enables us to identify and evaluate the functional role of feedback connections between cortical areas in the context of texture processing, namely the suppression of ambiguous cell activities leading to a sharply localized detection of texture boundaries. One of the likely neural origins of modulatory effects on V1 cell activation levels, as observed in electrophysiological studies using single- and multi-unit recordings, can be **resolved**.

L7 ANSWER 23 OF 65 PASCAL COPYRIGHT 2009 INIST-CNRS. ALL RIGHTS Full Text
RESERVED. on STN DUPLICATE 3
AN 2004-0207387 PASCAL
CP Copyright © 2004 INIST-CNRS. All rights reserved.
TIEN Design and implementation of the multilingual product retrieval agent through XML and the Semantic networks in EC
Service-oriented computing : Trento, 15-18 December 2003
AU MOON Yoo-Jin; KIJOON CHOI; KYONGHO MIN; WAN PYONG KIM; YOUNGHO HWANG; PANKOO KIM; YOUNGSE MUN
ORLOWSKA Maria E. (ed.); WEERAWARANA Sanjiva (ed.); PAPAZOGLOU Michael P. (ed.); JIAN YANG (ed.)
CS MIS Department, Hankuk University of Foreign Studies, 270 Imun-dong Tongdaemun-Gu, Seoul 130-791, Korea, Republic of; School of Computer and Information Sciences, Auckland University of Technology, Auckland 1020, New Zealand; Kunsan University, Kunsan, Cheonbuk 573-701, Korea, Republic of; Chosun University, Kwangju 506-741, Korea, Republic of; Korea National Defense University, Seoul 122-875, Korea, Republic of
SO Lecture notes in computer science, (2003), 2910, 423-433, 21 refs.
Conference: 1 ICSOC 2003 : international conference on service-oriented computing, Trento (Italy), 15 Dec 2003
ISSN: 0302-9743
ISBN: 3-540-20681-7
DT Journal; Conference
BL Analytic
CY Germany, Federal Republic of
LA English
AV INIST-16343, 354000117814170290
AB Retrieval for products is an important task for e-commerce, since it represents an interface of the customer contact to e-commerce. And e-commerce should provide customers with easily accessible processes in searching. Especially, the product **information** on the World Wide Web needs integration and standardization to keep the pace of rapid expansion with wide reachable ranges. International standards on product catalogs are converging on UNSPSC (Universal Standard Products and Services Classification). With adoption of this standard, we designed the **architecture** of a multilingual product retrieval agent. The **architecture** is based on the central repository model of product catalog management with a distributed updating process. It also includes the perspectives of buyers and suppliers. In addition, the consistency and version management of product **information** are controlled by UNSPSC. The multilingual product **names** are **resolved** by semantic networks, a thesaurus, and product **name** ontology, which enable the present **architecture** to be expanded to the Semantic Web applications.

L7 ANSWER 24 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on Full Text
STN
AN 2003:314561 BIOSIS
DN PREV200300314561
TI Phylogeny and evolution of calcareous sponges: Monophyly of Calcinea and Calcaronea, high level of morphological homoplasy, and the primitive nature of axial symmetry.

AU Manuel, Michael [Reprint Author]; Borchiellini, Carole; Alivon, Eliane; Le Parco, Yannick; Vacelet, Jean; Boury-Esnault, Nicole
CS Centre d'Oceanologie de Marseille, Station Marine d'Endoume, UMR-CNRS 6540 DIMAR, Universite de la Mediterranee, rue de la Batterie des Lions, 13007, Marseille, France
michael.manuel@snv.jussieu.fr
SO Systematic Biology, (June 2003) Vol. 52, No. 3, pp. 311-333. print.
ISSN: 1063-5157 (ISSN print).
DT Article
LA English
ED Entered STN: 9 Jul 2003
Last Updated on STN: 9 Jul 2003
AB Because calcareous sponges are triggering renewed interest with respect to basal metazoan evolution, a phylogenetic framework of their internal relationships is needed to clarify the evolutionary history of key morphological characters. Morphological variation was scored at the suprageneric level within Calcispongia, but little phylogenetic **information** could be retrieved from morphological characters. For the main subdivision of Calcispongia, the analysis of morphological data weakly supports a classification based upon cytological and embryological characters (Calcinea/Calcaronea) rather than the older classification scheme based upon the aquiferous system (Homocoela/Heterocoela). The 18S ribosomal RNA data were then analyzed, both alone and in combination with morphological characters. The monophyly of Calcispongia is highly supported, but the position of this group with respect to other sponge lineages and to eumetazoan taxa is not **resolved**. The monophyly of both Calcinea and Calcaronea is retrieved, and the data strongly rejected the competing Homocoela/Heterocoela hypothesis. The phylogeny implies that characters of the skeleton **architecture** are highly homoplastic, as are characters of the aquiferous system. However, axial symmetry seems to be primitive for all Calcispongia, a conclusion that has potentially far-reaching implications for hypotheses of early body plan evolution in Metazoa.

L7 ANSWER 25 OF 65 AQUASCI COPYRIGHT 2009 FAO (On behalf of the
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ASFA Advisory Board). All rights reserved. on STN DUPLICATE 4
AN 2005:1912 AQUASCI
DN ASFA2 2005
TI An ERP approach for container terminal operating systems
AU Choi, H.R.; Kim, H.S.; Park, B.J.; Park, N.-K.; Lee, S.W.
CS Department of MIS, Dong-A University 840, Hadan-dong, Saha-gu, Busan 604-714, Korea
SO Maritime Policy & Management [Marit. Policy Manage.], (20030900) vol. 30, no. 3, pp. 197-210.
ISSN: 0308-8839.
DT Journal
FS ASFA2
LA English
SL English
AB The major characteristics of ERP (Enterprise Resource Planning) are an enterprise-wide system that covers all the business functions and **information** resources, integrated database, built-in best industry practice, packaged software and open **architecture**. ERP enables reduction of system development time, flexibility, standardization of workflow and effective business planning capability. ERP is mainly for the manufacturing industry. However, the principles of ERP can also be applied to container terminal operating systems. This paper presents an ERP system approach for a container terminal. It has clustered the workflow of a container terminal and analysed the business process to generate the best workflows. The integrated database is designed to eliminate redundancy and keep integration. The core of ERP for container terminal is the planning facility such as berth planning and yard planning. The planning capability is very tightly coupled with data flow from client **entities** such as shipping companies. The ERP can handle the existing problems of container terminal operation that are mainly caused by lack of integration of a whole **information** resource in a container terminal, ad-hoc and poor planning capability, disconnected and incorrect data from client companies. The ERP approach can not only **resolve** the problems of container terminals but also promote adoption of **information** systems for container terminals in the world that have not yet implemented terminal operating systems.

L7 ANSWER 26 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on Full Text
STN
AN 2003:508844 BIOSIS
DN PREV200300509044
TI Detection of novel tetracycline resistance gene sequences in soil treated with swine manure.
AU Rodriguez-Minguela, C. M. [Reprint Author]; Tiedje, J. M. [Reprint Author]; Jacobs, L. W. [Reprint Author]
CS Michigan State University, East Lansing, MI, USA
SO Abstracts of the General Meeting of the American Society for Microbiology, (2003) Vol. 103, pp. A-042.
http://www.asmusa.org/mtgsrc/generalmeeting.htm. cd-rom.
Meeting Info.: 103rd American Society for Microbiology General Meeting. Washington, DC, USA. May 18-22, 2003. American Society for Microbiology.
ISSN: 1060-2011 (ISSN print).
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 29 Oct 2003
Last Updated on STN: 29 Oct 2003
AB Understanding the origin and fate of antibiotic resistance requires understanding genetic reservoirs that are not only found in the easily cultured clinical strains. We used a culture-independent approach to detect novel tetracycline resistance genes coding for ribosomal protection proteins (RPP) in DNA from manured soils. We chose tetracycline as the model since it is widely used in animal agriculture as a growth promoter. DNA was extracted from composite soil samples obtained from eight farms having different histories of swine manure application as well as from nearby control soils that had no manure application. Degenerate primers corresponding to a conserved 1.3kb region were used to target nucleotide sequences of RPP determinants. These were only detected in samples from a field to which pig manure of animals feed with tetracycline as a growth promoter was recently applied. Soil samples nearby but from where no manure was used yielded no RPP PCR products. Putative RPP genes were cloned and selected sequenced. Based on current conventions for the classification of RPP's, the analyzed clones were affiliated to other previously described determinants. Complete identity to published RPP sequences was observed only in three instances. Two clones had potential novel genotypes with amino acid sequence identities of 70 and 59% to Tet 32 and Tet Q, respectively, while a third clone showed 84% amino acid sequence identity to Tet W and emerged as a putative new variant of this determinant. All partial amino acid sequences contained a GTP-binding domain **architecture** very similar to that of previously described RPP's. PCR products could readily be detected only in recently manured soils suggesting that the resistance gene load is reduced under field conditions. This study suggests that potentially novel sequences of RPP genes can be recovered from environmental DNA, which would expand extant diversity among this gene family, which is largely derived from isolates. This **information** and approach should provide a better understanding of the ecology of antibiotic resistance genes, and will help **resolve** to what degree isolate based studies are lacking.

L7 ANSWER 27 OF 65 PASCAL COPYRIGHT 2009 INIST-CNRS. ALL RIGHTS RESERVED. on STN Full Text
AN 2003-0082642 PASCAL
CP Copyright © 2003 INIST-CNRS. All rights reserved.
TIEN Channel islands in a reflective ocean: Large scale event distribution in heterogeneous networks
NETWORKiNG 2002 : networking technologies, services, and protocols ; performance of computer and communication networks ; mobile and wireless communications : Pisa, 19-24 May 2002
AU CROWCROFT Jon
GREGORI Enrico (ed.); CONTI Marco (ed.); CAMPBELL Andrew T. (ed.); OMIDYAR Guy (ed.); ZUKERMAN Moshe (ed.)
CS University of Cambridge, Computer Laboratory, William Gates Building, J J Thomson Avenue, Cambridge CB3 0FD, United Kingdom
SO Lecture notes in computer science, (2002), 2345, 1-9, 41 refs.
Conference: 2 International IFIP-TC6 networking conference, Pisa (Italy), 19 May 2002

ISSN: 0302-9743
ISBN: 3-540-43709-6
DT Journal; Conference
BL Analytic
CY Germany, Federal Republic of
LA English
AV INIST-16343, 354000108472840010
AB This is a discussion paper about the possible future use of network and transport level multicast services to support extremely large scale event distribution. To date, event notification services[40] have been limited in their scope due to limitations of the infrastructure At the same time, Internet network and transport layer multicast services have seen limited deployment due to lack of user demand (with the exception more recently of streaming services, e.g. on Sprint's US core network, and in the Internet II). Recent research in active and reflective middleware suggests a way to **resolve** these two problems at one go. Event-driven and messaging infrastructures are emerging as the most flexible and feasible solution for enabling rapid and dynamic integration of legacy and monolithic software applications into distributed systems. Event infrastructures also support deployment and evolution of traditionally difficult-to-build active systems such as large-scale collaborative environments and mobility aware **architectures**. Event notification is concerned with propagation of state changes in objects in the form of events. A crucial aspect of events is that they occur asynchronously. Event consumers have no control over when events are triggered. On the other hand, event suppliers do not generally know what **entities** might be interested in the events they provide. These two aspects clearly define event notification as a model of asynchronous and de-coupled communication, where **entities** communicate in order to exchange **information**, but do not directly control each other. The IETF is just finishing specifying a family of reliable multicast transport protocols, for most of which there are pilot implementations. Key amongst these for the purposes of this research is the exposure to end systems of router filter functionality in a programmable way, known as Generic Router Assist. This is an inherent part of the Pragmatic General Multicast service, implemented by Reuters, Tibco and Cisco in their products, although it has not been widely known or used outside of the TIBNET products until very recently.

L7 ANSWER 28 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
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STN
AN 2003:293720 BIOSIS
DN PREV200300293720
TI IMAGING Ca!2+ FLUX THROUGH SINGLE N - TYPE VOLTAGE - GATED Ca2+ CHANNELS EXPRESSED IN XENOPUS OOCYTES.
AU Demuro, A. [Reprint Author]; Parker, I. [Reprint Author]
CS Neurobiology and Behavior, Univ CA Irvine, Irvine, CA, USA
SO Society for Neuroscience Abstract Viewer and Itinerary Planner, (2002) Vol. 2002, pp. Abstract No. 312.2. http://sfn.scholarone.com. cd-rom. Meeting Info.: 32nd Annual Meeting of the Society for Neuroscience. Orlando, Florida, USA. November 02-07, 2002. Society for Neuroscience.
DT Conference; (Meeting)
Conference; (Meeting Poster)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 25 Jun 2003
Last Updated on STN: 25 Jun 2003
AB The introduction of patch-clamp recording revolutionized our ability to study the functioning of individual ion channels. Nevertheless, patch-clamp recording suffers some limitations. Channels must be physically accessible to the pipette and seal formation may disrupt local cellular **architecture**; recordings are obtained from only one channel at a time; and it is difficult to change solution in the pipette. We describe the potential of fluorescence microscopy as an advantageous adjunct to study single ion channel activity. Visualization of Ca2+ influx through individual N-type Ca2+ channels transiently expressed in Xenopus oocytes was carried out using confocal microscopy to image along the scan line in the plane of the membrane. Step depolarizations (20-+30 mV) delivered by a two electrode voltage clamp produced local (< 0.6 mum) calcium signals representing stochastic openings of multiple discrete channels along the scan line. Single channel calcium transients (SCCATs)

as brief as 10 ms could be **resolved**, and we were able to determine channel lifetime and latency distributions.)Confocal fluorescence imaging thus provides temporal **information** on channel gating similar to that obtained by patch-clamp recording. Moreover, optical imaging provides spatial **information** from multiple channels, involves minimal disruption and is applicable to channels that are not accessible to a patch pipette. We believe that optical single-channel recording will find many applications for study of the numerous voltage-and ligand-gated channels that have appreciable Ca2+ permeability.

L7 ANSWER 29 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on Full Text
STN
AN 2001:489246 BIOSIS
DN PREV200100489246
TI Integrated exposure and dose modeling and analysis system. 3. Deposition of inhaled particles in the human respiratory tract.
AU Lazaridis, Mihalis; Broday, David M.; Hov, Oystein; Georgopoulos, Panos G. [Reprint author]
CS Rutgers University and UMDNJ, Piscataway, NJ, USA
panosg@fidelio.rutgers.edu
SO Environmental Science and Technology, (September 15, 2001) Vol. 35, No. 18, pp. 3727-3734. print.
CODEN: ESTHAG. ISSN: 0013-936X.
DT Article
LA English
ED Entered STN: 17 Oct 2001
Last Updated on STN: 23 Feb 2002
AB Detailed **information** on the composition-**resolved** size distribution of particulate matter deposited along the human respiratory tract can help linking epidemiological, toxicological, and pathological studies and thus potentially improve the understanding of the origin of pulmonary disorders induced by respirable pathogens. For this purpose, a new mechanistic dosimetry model describing the dynamics of respirable particles in the human airways was developed. Model predictions of transport and fate of inhaled aerosols are based on solutions of the aerosol general dynamic equation, which describes changes in particle size and mass distributions resulting from processes such as nucleation, condensation, coagulation, gas phase chemical reaction, and deposition. To compensate for approximating the three-dimensional problem by considering only axial variations along the airways, boundary layer effects are introduced via appropriate dimensionless transport parameters. The **architecture** of the human lung is described by Weibel's simple regular dichotomous model. An important advantage of the present approach is that it allows testing the significance of intersubject lung morphology and ventilation variability for particle deposition and dose calculations. The model predicts the evolution of size and composition distributions of inhaled particles and the deposition profile along the human lower respiratory tract: in general, model predictions are in qualitative and quantitative agreement with tracheobronchial and alveolar deposition data.

L7 ANSWER 30 OF 65 PASCAL COPYRIGHT 2009 INIST-CNRS. ALL RIGHTS Full Text
RESERVED. on STN DUPLICATE 5
AN 2001-0339569 PASCAL
CP Copyright © 2001 INIST-CNRS. All rights reserved.
TIEN The role of satellites in global IT: Trends and implications
Multimedia Communications over Satellites
AU JAMALIPOUR Abbas; TUNG Tracy
SALKINTZIS Apostolis K. (ed.)
CS The University of Sydney, United States
SO IEEE personal communications, (2001), 8(3), 5-11, 16 refs.
ISSN: 1070-9916 CODEN: IPCME7
DT Journal
BL Analytic
CY United States
LA English
AV INIST-26674, 354000096496590010
AB Satellite will continue to be an essential element in the establishment of long-distance telecommunications for many years, and it will have a major role in the implementation of the so-called global **information** infrastructure in the future. This is because of the particular feature

of the satellite that can provide wide coverage independent of the actual land distance between any pair of communicating **entities**. The new generation of broadband satellite systems, which can provide high-speed data transmission and connectivity to terrestrial data networks, will create profound changes in all aspects of the emerging data communications applications such as Internet and electronic commerce. In this article we explore characteristics of the future satellite networks and their interoperability with terrestrial wireless and wired networks. The emerging data and IP applications impose new implementation issues on the long-latency and restricted satellite channel that must be **resolved** before such interoperability between satellite and terrestrial networks takes place.

L7 ANSWER 31 OF 65 DISSABS COPYRIGHT (C) 2009 ProQuest Information Full Text
and Learning Company; All Rights Reserved on STN
AN 2001:24697 DISSABS Order Number: AAI9984989
TI Establishing the performance impact of persistent, location-independent, identification of resources in distributed systems
AU Stewart, Darin Lewis [Ph.D.]; Williams, James G. [adviser]
CS University of Pittsburgh (0178)
SO Dissertation Abstracts International, (2000) Vol. 61, No. 9B, p. 4830. Order No.: AAI9984989. 145 pages.
ISBN: 0-599-91879-9.
DT Dissertation
FS DAI
LA English
AB Uniform Resource **Names** (URN), or more generally Persistent, Location-independent Identifiers (PLIs) promise to **resolve** many of the long-standing challenges of resource management in distributed systems. Chief among these problems is the issue of "dead links." Once an **Information** Bearing Object has been registered with a PLI scheme, its availability is, theoretically, assured in perpetuity. The reliability of resource availability implied by this has prompted many system implementers to go to great pains to facilitate inclusion of PLIs, in one form or another, in their **architectures**.

These decisions seem to be based more on faith, enthusiasm, and wishful thinking than on any rational analysis. This is due to the fact that with all of the work and experimentation that has gone into PLIs, the cost of adding persistent identification to a system has yet to be addressed. The availability of such a metric would seem to be essential to making an informed decision on whether and to what extent to adopt such a scheme.

This study examined the retrieval performance of the three currently deployed PLI solutions, the URN-based Object Handle system, Persistent, Uniform Resource Locators (PURL) and System Wide Identifiers for Location Look-up (SWILL). Times were logged for each aspect of the resource resolution location process and analyzed to determine the relative impact of each scheme on retrieval performance in a distributed system. These results where then used to inform the modeling of the resolution process.

This study has shown that contrary to the claims of the producers of PLI resolution schemes there is in fact a dramatic degradation of performance when these systems are integrated into an IT **architecture**. It has been shown that this performance degradation can increase retrieval time by up to a factor of 22, which is clearly not acceptable in a production system.

It has also been shown that there are several discreet factors within both PLI scheme implementation and deployment, which can mitigate this performance degradation. To demonstrate these factors and to provide a means to determine the optimum approach to their development, a queueing network model has been developed and demonstrated.

L7 ANSWER 32 OF 65 NTIS COPYRIGHT 2009 NTIS on STN
AN 2007(13):00135 NTIS Order Number: ADA461095/XAB
TI Generalized Aliasing as a Basis for Program Analysis Tools. Doctoral thesis.
AU O'Callahan, R.
CS Carnegie-Mellon Univ., Pittsburgh, PA. School of Computer Science. (005343049 423887)
NR ADA461095/XAB; CMU-CS-01-124
295p; Nov 2000
NC Contract(s): F33615-03-1-1330 , F30602-97-2-0031

DT Dissertation
CY United States
LA English
NTE Sponsored in part by the National Science Foundation under Grant No., CCR9523972.
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OS GRA&I0713
AB Tools for automatic program analysis promise to improve programmer productivity by searching and summarizing large bodies of code. However, the phenomenon of aliasing different **names** being used to refer to the same data reduces the effectiveness of simple textual analyses. This dissertation describes the design of a system, Ajax, that addresses this problem by using semantics-based program analysis as the basis for a number of different tools to aid Java programmers. To enable the construction of many tools, Ajax imposes a clean separation between analysis engines that produce alias **information** and tools that consume it. Analyses are treated as 'black boxes' satisfying a simple, formal specification given in terms of the semantics of Java bytecode. Knowing only this specification, one can build many different tools with only a small amount of code. The thesis explores the flexibility and efficiency of the design by describing the construction and evaluation of several different tools: tools to find dead code, **resolve** Java virtual method calls, statically check Java downcasts, search for accesses to objects, and build object models. To support these tools, Ajax includes a novel static analysis engine for Java called SEMI, based on type inference with polymorphic recursion. SEMI provides fully context sensitive analysis of large programs. Using SEMI with the downcast checking tool, Ajax can prove the safety of more than 50% of the downcast instructions in some real-life Java programs, such as Sun's bytecode disassembler and the JavaCC parser generator. Ajax is the first system to address this particular task. One of the key goals of this thesis is to study issues bearing on the practical utility of static analysis tools for programmers. This document describes some of the challenges involved in building an analysis system for off-the-shelf Java applications, and suggests some possible avenues for future research.

L7 ANSWER 33 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
Full Text
STN
AN 2001:12422 BIOSIS
DN PREV200100012422
TI Multisite fluorescence in proteins with multiple tryptophan residues. Apomyoglobin natural variants and site-directed mutants.
AU Tcherkasskaya, Olga [Reprint author]; Bychkova, Valentina E.; Uversky, Vladimir N.; Gronenborn, Angela M.
CS Laboratory of Experimental and Computational Biology, NCI, National Institutes of Health, Bethesda, MD, 20892, USA
tcherkasskaya@nih.gov
SO Journal of Biological Chemistry, (Novemeber, 2000) Vol. 275, No. 46, pp. 36285-36294. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
ED Entered STN: 27 Dec 2000
Last Updated on STN: 27 Dec 2000
AB Time-**resolved** fluorescence experiments were carried out on a variety of apomyoglobins with one or two tryptophan (Trp) residues located at invariant positions 7 and 14 in the primary sequence. In all cases, the Trp fluorescence kinetics were **resolved** adequately into two discrete lifetime domains, and decay-associated spectra (DAS) were obtained for each decay component. The DAS **resolved** for unfolded proteins were indistinguishable by position of the emission maxima and the spectral shapes. The folded proteins revealed noticeable differences in the DAS, which relate to the diverse local environments around the Trp residues in the individual proteins. Furthermore, the DAS of wild-type protein possessing two Trp residues were simulated well by that of one Trp mutants either in the native, molten globule, or unfolded states. Overall, employing Trp fluorescence and site-directed mutagenesis allowed us to

highlight the conformational changes induced by the single amino acid replacement and generate novel structural **information** on equilibrium folding intermediates. Specifically, it was found that conformational fluctuations in the local cluster around the evolutionarily conserved Trp14 are very similar in the native and molten globule states of apomyoglobins. This result indicates that residues in the E and B helices contributing to this cluster are most likely involved in the stabilization of the overall **architecture** of the structured molten globule intermediate.

L7 ANSWER 34 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on Full Text
STN
AN 2000:421012 BIOSIS
DN PREV200000421012
TI Vegetative and reproductive innovations of early land plants: Implications for a unified phylogeny.
AU Renzaglia, Karen Sue [Reprint author]; Duff, R. Joel; Nickrent, Daniel L. [Reprint author]; Garbary, David J.
CS Department of Plant Biology and Center for Systematic Biology, Southern Illinois University, Carbondale, IL, 62901-6509, USA
SO Philosophical Transactions of the Royal Society of London B Biological Sciences, (29 June, 2000) Vol. 355, No. 1398, pp. 769-793. print. ISSN: 0962-8436.
DT Article
LA English
ED Entered STN: 4 Oct 2000
Last Updated on STN: 8 Jan 2002
AB As the oldest extant lineages of land plants, bryophytes provide a living laboratory in which to evaluate morphological adaptations associated with early land existence. In this paper we examine reproductive and structural innovations in the gametophyte and sporophyte generations of hornworts, liverworts, mosses and basal pteridophytes. Reproductive features relating to spermatogenesis and the **architecture** of motile male gametes are overviewed and evaluated from an evolutionary perspective. Phylogenetic analyses of a data set derived from spermatogenesis and one derived from comprehensive morphogenetic data are compared with a molecular analysis of nuclear and mitochondrial small subunit rDNA sequences. Although relatively small because of a reliance on water for sexual reproduction, gametophytes of bryophytes are the most elaborate of those produced by any land plant. Phenotypic variability in gametophytic habit ranges from leafy to thalloid forms with the greatest diversity exhibited by hepatics. Appendages, including leaves, slime papillae and hairs, predominate in liverworts and mosses, while hornwort gametophytes are strictly thalloid with no organized external structures. Internalization of reproductive and vegetative structures within mucilage-filled spaces is an adaptive strategy exhibited by hornworts. The formative stages of gametangial development are similar in the three bryophyte groups, with the exception that in mosses apical growth is intercalated into early organogenesis, a feature echoed in moss sporophyte ontogeny. A monosporangiate, unbranched sporophyte typifies bryophytes, but developmental and structural innovations suggest the three bryophyte groups diverged prior to elaboration of this generation. Sporophyte morphogenesis in hornworts involves non-synchronized sporogenesis and the continued elongation of the single sporangium, features unique among archegoniates. In hepatics, elongation of the sporophyte seta and archegoniophore is rapid and requires instantaneous wall expandability and hydrostatic support. Unicellular, spiralled elaters and capsule dehiscence through the formation of four regular valves are autapomorphies of liverworts. Sporophytic sophistications in the moss clade include conducting tissue, stomata, an assimilative layer and an elaborate peristome for extended spore dispersal. Characters such as stomata and conducting cells that are shared among sporophytes of mosses, hornworts and pteridophytes are interpreted as parallelisms and not homologies. Our phylogenetic analysis of three different data sets is the most comprehensive to date and points to a single phylogenetic solution for the evolution of basal embryophytes. Hornworts are supported as the earliest divergent embryophyte clade with a moss/liverwort clade sister to tracheophytes. Among pteridophytes, lycophytes are monophyletic and an assemblage containing ferns, Equiselum and psilophytes is sister to seed plants. Congruence between morphological and molecular hypotheses indicates that these data sets are tracking the same phylogenetic signal and reinforces our phylogenetic conclusions. It appears that total

evidence approaches are valuable in **resolving** ancient radiations such as those characterizing the evolution of early embryophytes. More **information** on land plant phylogeny can be found at: http://www.science.siu.edu/landplants/index.html.

L7 ANSWER 35 OF 65 SCISEARCH COPYRIGHT (c) 2009 The Thomson Full Text
Corporation on STN
AN 2001:545086 SCISEARCH
GA The Genuine Article (R) Number: 449LC
TI Application-layer anycasting: A server selection **architecture** and use in a replicated web service
AU Zegura E W (Reprint)
CS Georgia Inst Technol, Coll Comp, Atlanta, GA 30332 USA (Reprint)
AU Ammar M H; Fei Z; Bhattacharjee S
CS Univ Maryland, Dept Comp Sci, College Pk, MD 20742 USA
CYA USA
SO IEEE-ACM TRANSACTIONS ON NETWORKING, (AUG 2000) Vol. 8, No. 4, pp. 455-466.
ISSN: 1063-6692.
PB IEEE-INST ELECTRICAL ELECTRONICS ENGINEERS INC, 345 E 47TH ST, NEW YORK, NY 10017-2394 USA.
DT Article; Journal
LA English
REC Reference Count: 30
ED Entered STN: 20 Jul 2001
Last Updated on STN: 20 Jul 2001
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB Server replication improves the ability of a service to handle a large number of clients. One of the important factors in the efficient utilization of replicated servers is the ability to direct client requests to the "best" server, according to some optimality criteria, In the anycasting communication paradigm, a sender communicates with a receiver chosen from an anycast group of equivalent receivers. As such, anycasting is well suited to the problem of directing clients to replicated servers.
This paper examines the definition and support of the anycasting paradigm at the application layer, providing a service that uses an anycast **resolver** to map an anycast domain **name** and a selection criteria into an TP address. By realizing anycasting in the application layer, we achieve flexibility in the optimization criteria and ease the deployment of the service.
As a case study, we examine the performance of our system for a key service: replicated web servers. To this end, we develop an approach for estimating the response time that a client will experience when accessing given servers, Such **information** is maintained in the anycast **resolver** that clients query to obtain the identity of the server with the best estimated response time. Our performance collection technique combines server push with **resolver** probes to estimate the expected response time without undue overhead, Our experiments show that selecting a server using our **architecture** and estimation technique can improve the client response time by a factor of two over nearest server selection and by a factor of four over random server selection.

L7 ANSWER 36 OF 65 SCISEARCH COPYRIGHT (c) 2009 The Thomson Full Text
Corporation on STN
AN 2000:630378 SCISEARCH
GA The Genuine Article (R) Number: 342VE
TI Interaction devices for coordinating cooperative distributed systems
AU Ghenniwa H (Reprint)
CS Univ Western Ontario, Dept Elect & Comp Engn, Cooperat Distributed Syst Engn Grp, London, ON N6G 1H1, Canada (Reprint)
AU Kamel M
CS Univ Waterloo, Dept Syst Design Engn, Pattern Anal & Machine Intelligence Lab, Waterloo, ON N2L 3G1, Canada
CYA Canada
SO INTELLIGENT AUTOMATION AND SOFT COMPUTING, (2000) Vol. 6, No. 3, pp. 173-184.
ISSN: 1079-8587.
PB AUTOSOFT PRESS, PO BOX 14126, ALBUGUERQUE, NM 87191-4126 USA.
DT Article; Journal
LA English

REC Reference Count: 24
ED Entered STN: 2000
Last Updated on STN: 2000
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB A cooperative distributed systems approach is an appropriate design paradigm for many applications, such as manufacturing control and network management. A fundamental problem in this paradigm is how to manage the interdependencies among the **entities**. The solution to this interdependency problem is called coordination. In this paper, coordination has been described in terms of structure and mechanism. This paper focuses on the mechanism aspect of the coordination. It is viewed as a composition of decision points and interaction devices directed to deal with different aspects of the interdependency problem. This paper also provides a coordinated, intelligent rational agent (CIR-Agent) model for cooperative distributed systems. The structure and the **architecture** of the agent are based on its mental state regarding achieving a goal. The agent's structure consists of four main components: problem-solver, pre-interaction, interaction, and execution. There is no global control of coordination allowed in the proposed model, for which the agents utilize different interaction devices to **resolve** their interdependencies.

L7 ANSWER 37 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on Full Text
STN
AN 1999:135109 BIOSIS
DN PREV199900135109
TI Biochemical characterization and solution structure of nitrous oxide reductase from Alcaligenes xylosoxidans (NCIMB 11015).
AU Ferretti, Silvia; Grossmann, J. Guenter; Hasnain, S. Samar; Eady, Robert R.; Smith, Barry E. [Reprint author]
CS Nitrogen Fixation Lab., John Innes Centre, Norwich Res. Park, Colney, Norwich NR4 7UH, UK
SO European Journal of Biochemistry, (Feb., 1999) Vol. 259, No. 3, pp. 651-659. print.
CODEN: EJBCAI. ISSN: 0014-2956.
DT Article
LA English
ED Entered STN: 31 Mar 1999
Last Updated on STN: 31 Mar 1999
AB Nitrous oxide reductase (N2OR) is the terminal enzyme involved in denitrification by microbes. No three-dimensional structural **information** has been published for this enzyme. We have isolated and characterized N2OR from Alcaligenes xylosoxidans (AxN2OR) as a homodimer of Mr 134 000 containing seven to eight copper atoms per dimer. Comparison of sequence and compositional data with other N2ORs suggests that AxN2OR is typical and can be expected to have similar domain folding and subunit structure to other members of this family of enzymes. We present synchrotron X-ray-scattering data, analysed using a model-independent method for shape restoration, which gave a apprxeq 20 ANG resolution structure of the enzyme in solution, providing a glimpse of the structure of any N2OR and shedding light on the molecular **architecture** of the molecule. The specific activity of AxN2OR was apprxeq 6 mumol of N2O reducedcntdotmin-1cntdot(mg of protein)-1; N2OR activity showed both base and temperature activation. The visible spectrum exhibited an absorption maximum at 550 nm with a shoulder at 635 nm. On oxidation with K3Fe(CN)6, the absorption maximum shifted to 540 nm and a new shoulder at 480 nm appeared. Reduction under anaerobic conditions resulted in the formation of an inactive blue form of the enzyme with a broad absorption maximum at 650 nm. As isolated, the enzyme shows an almost featureless EPR spectrum, which changes on oxidation to give an almost completely **resolved** seven-line hyperfine signal in the gII region, g = 2.18, with AII = 40 G, consistent with the enzyme being partially reduced as isolated. Both the optical and EPR spectra of the oxidized enzyme are characteristic of the presence of a CuA centre.

L7 ANSWER 38 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on Full Text
STN
AN 1999:304973 BIOSIS
DN PREV199900304973
TI Laser-scanning cytometry: A new instrumentation with many applications.
AU Darzynkiewicz, Zbigniew [Reprint author]; Bedner, Elzbieta; Li, Xun;

Gorczyca, Wojciech; Melamed, Myron R.
CS Brander Cancer Research Institute, New York Medical College, 19 Bradhurst Ave., Hawthorne, NY, 10532, USA
SO Experimental Cell Research, (May 25, 1999) Vol. 249, No. 1, pp. 1-12. print.
CODEN: ECREAL. ISSN: 0014-4827.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 12 Aug 1999
Last Updated on STN: 12 Aug 1999
AB The laser-scanning cytometer (LSC) is a microscope-based cytofluorometer which has attributes of both flow and image cytometry. Laser-excited fluorescence emitted from fluorochromed individual cells on a microscope slide is measured at multiple wavelengths rapidly with high sensitivity and accuracy. Though the instrument has been available commercially for only 3 years, it is already used in a variety of different applications in many laboratories. This review focuses on the following unique analytical capabilities of LSC which complement those of flow cytometry and fluorescence image analysis: (a) the cells are positioned on slides during measurement so they may be examined repeatedly over time, a feature useful for studies of enzyme kinetics and other time-**resolved** processes; (b) sequential analysis of the same cells can be carried out using different immuno- or cytochemical stains or genetic probes, merging **information** on cell immunophenotype, cell functions, expression of particular proteins, DNA ploidy and cell cycle position, and/or cytogenetic profile for each measured cell; (c) any of the cells measured can be relocated to correlate with visual examination by fluorescence or brightfield microscopy or with any other parameter; (d) topographic distribution of fluorescence measurements within the cell, in cytoplasm vs nucleus, permits analysis of the translocation of regulatory molecules such as NFkappaB, p53, etc., and is essential for FISH analysis; (e) hyperchromicity of nuclear DNA as measured by maximal pixel fluorescence intensity allows one to identify cell types differing in degree of chromatin condensation such as mitotic or apoptotic cells; (f) analysis of tissue section **architecture** and of the constituents in transected cells within tissue sections by ratiometric assays normalized to DNA content extends applications of LSC in clinical pathology; (g) because cell loss during sample preparation and staining is minimal, samples with a paucity of cells canbe analyzed; and (h) analyzed cells can be stored indefinitely, e.g., for archival preservation or additional analysis. Potential future applications of LSC are discussed.

L7 ANSWER 39 OF 65 MEDLINE on STN
Full Text
AN 1999032369 MEDLINE
DN PubMed ID: 9817431
TI Leonardo da Vinci: the search for the soul.
AU Del Maestro R F
CS Division of Neurosurgery, London Health Sciences Centre, University of Western Ontario, Canada.. valerie.denomme@lhsc.on.ca
SO Journal of neurosurgery, (1998 Nov) Vol. 89, No. 5, pp. 874-87. Ref: 46
Journal code: 0253357. ISSN: 0022-3085.
CY United States
DT Biography
Historical
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
LA English
FS Abridged Index Medicus Journals; Priority Journals; History of Medicine
EM 199812
ED Entered STN: 15 Jan 1999
Last Updated on STN: 3 Mar 2000
Entered Medline: 4 Dec 1998
AB The human race has always contemplated the question of the anatomical location of the soul. During the Renaissance the controversy crystallized into those individuals who supported the heart ("cardiocentric soul") and others who supported the brain ("cephalocentric soul") as the abode for this elusive **entity**. Leonardo da Vinci (1452-1519) joined a long list of other explorers in the "search for the soul." The method he used to **resolve** this anatomical problem involved the accumulation of **information** from ancient and contemporary sources, careful notetaking, discussions with acknowledged experts, and his own personal search for the

truth. Leonardo used a myriad of innovative methods acquired from his knowledge of painting, sculpture, and **architecture** to define more clearly the site of the "senso comune"--the soul. In this review the author examines the sources of this ancient question, the knowledge base tapped by Leonardo for his personal search for the soul, and the views of key individuals who followed him.

L7 ANSWER 40 OF 65 PASCAL COPYRIGHT 2009 INIST-CNRS. ALL RIGHTS
Full Text
RESERVED. on STN DUPLICATE 6
AN 1998-0533676 PASCAL
CP Copyright © 1998 INIST-CNRS. All rights reserved.
TIEN Leonardo da Vinci : the search for the soul
AU DEL MAESTRO R. F.
CS Brain Research Laboratories, Division of Neurosurgery, London Health Sciences Centre, University of Western Ontario, London, Ontario, Canada
SO Journal of neurosurgery, (1998), 89(5), 874-887, 46 refs.
ISSN: 0022-3085 CODEN: JONSAC
DT Journal
BL Analytic
CY United States
LA English
AV INIST-6023, 354000071364770280
AB The human race has always contemplated the question of the anatomical location of the soul. During the Renaissance the controversy crystallized into those individuals who supported the heart ("cardiocentric soul") and others who supported the brain ("cephalocentric soul") as the abode for this elusive **entity**. Leonardo da Vinci (1452-1519) joined a long list of other explorers in the "search for the soul." The method he used to **resolve** this anatomical problem involved the accumulation of **information** from ancient and contemporary sources, careful notetaking, discussions with acknowledged experts, and his own personal search for the truth. Leonardo used a myriad of innovative methods acquired from his knowledge of painting, sculpture, and **architecture** to define more clearly the site of the "senso comune"-the soul. In this review the author examines the sources of this ancient question, the knowledge base tapped by Leonardo for his personal search for the soul, and the views of key individuals who followed him.

L7 ANSWER 41 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
Full Text
STN
AN 1999:7566 BIOSIS
DN PREV199900007566
TI Pigment-pigment interactions in thylakoids and LHCII of chlorophyll a/c containing alga Pleurochloris meiringensis: Analysis of fluorescence-excitation and triplet-minus-singlet spectra.
AU Buechel, C.; Naqvi, K. Razi [Reprint author]; Melo, T. B.
CS Dep. Physics, Norwegian Univ. Science Technology, N-7034 Trondheim, Norway
SO Spectrochimica Acta Part A Molecular and Biomolecular Spectroscopy, (May, 1998) Vol. 54, No. 5, pp. 719-726. print.
ISSN: 1386-1425.
DT Article
LA English
ED Entered STN: 11 Jan 1999
Last Updated on STN: 11 Jan 1999
AB Time-**resolved** triplet-minus-singlet (TmS) difference spectra, DELTAA(lambda; t), fluorescence excitation spectra, X(lambda), and absorption spectra, A(lambda), are used for probing pigment-pigment interactions in the thylakoids (Chla/c-ThyI) and isolated light-harvesting complexes associated with photosystem II (Chla/c-LHCII) of the alga Pleurochloris meiringensis, whose chromophores comprise chlorophyll a (Chla), chlorophyll c (Chlc), and several carotenoids. The data provide **information** about interactions between Car*-and-Chla0, Chladag-and-Car0, Cardag-and-Chla0 (where the abbreviation Car stands for carotenoid, an asterisk and a dagger denote singlet and triplet excitation, respectively, and the superscript 0 denotes a molecule in the ground state). In Chla/c-ThyI, the efficiency of Car* fwdarw Chla* transfer (variant phiLH), determined by comparing A(lambda) and X(lambda), is slightly less than unity (ca. 0.85), whereas the efficiency of Chladag fwdarw Cardag transfer of triplet energy (variant phiTT) must be much closer to unity, since no long-lived Chladag could be detected; an interaction between Cardag and

Chla0, already familiar from investigations concerning the TmS spectra of the trimers and aggregates of Chla/b-LHCII (the light-harvesting complex associated with the photosystem II of higher plants), which manifests itself through a depletion signal (in the Qy region of Chla) decaying at the same rate as the Car TmS signal, is observed, and explained likewise. In Chla/c-LHCII, both efficiencies are found to be much lower; the drastic reduction in the two yields is attributed to the perturbation of the native molecular **architecture** of the complex by the detergent used in the isolation procedure. The overall TmS signal from Chla/c-LHCII can be decomposed into two contributions, DELTAA(lambda; t) = DELTA1A(lambda; t)+DELTA2A(lambda; t), where DELTA1A(lambda; t) with a lifetime of about 8 mus; DELTA2A(lambda; t), which persists for several hundred microseconds, is contributed by those Chladag molecules which fail to transfer their excitation to a Car neighbour. A comparison of DELTA1A(lambda; t) with the TmS signal of thylakoids shows differences which parallel those previously reported for the TmS spectra of trimers and aggregates of Chla/b-LHCII: the carotenoid peak at 510 nm is broader, and the Qy depletion signal larger, in the difference spectrum of thylakoids. The absorption spectrum of Chla/c-LHCII show no signs of Chla-Chla excitonic interactions, since the Chla-contribution to the spectrum can be reproduced well by simply red-shifting (by about 200 cm-1) the Q bands and the Soret band in the absorption spectrum of an ethanolic solution of Chla, an observation consistent with the absence, reported in a recent study, of excitonic band in the absorption spectrum of an ethanolic solution of Chla, an observation consistent with the absence, reported in a recent study, of excitonic bands in the circular dichroism spectrum of Chla/c-LHCII.

L7 ANSWER 42 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on Full Text
STN
AN 1998:510105 BIOSIS
DN PREV199800510105
TI Lessons learned from an Internet GP **information** system.
AU Briggs, J. S.; Bradley, M. P.
CS Object People, Sch. Computer Sci. Math., Univ. Portsmouth, Milton Campus, Locksway Rd., Southsea PO4 8JF, UK
SO Medical Informatics, (July-Sept., 1998) Vol. 23, No. 3, pp. 245-252. print.
ISSN: 0307-7640.
DT Article
LA English
ED Entered STN: 18 Dec 1998
Last Updated on STN: 18 Dec 1998
AB We describe the prototype of an application that in actual use would allow GPs to find out more **information** about consultants at hospitals. This would aid the GP in making the decision about which consultant a patient should be referred to. The requirements of the application from the GP's perspective are described, together with some of the issues that have to be **resolved** before hospitals can provide the necessary **information** in a standard format. The application is implemented as a client-server system using standard Internet technologies such as Java and HTML. This **architecture** has a number of advantages but also revealed some issues concerning security and the format of data, among other things. The project showed that there is a desire for such a system and that desire can be fulfilled at a relatively low cost.

L7 ANSWER 43 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on Full Text
STN
AN 1997:395612 BIOSIS
DN PREV199799694815
TI Static and dynamic membrane properties of large-terminal bipolar cells from goldfish retina: Experimental test of a compartment model.
AU Mennerick, Steven; Zenisek, David; Matthews, Gary [Reprint author]
CS Dep. Neurobiol. Behavior, SUNY Stony Brook, Stony Brook, NY 11794-5230, USA
SO Journal of Neurophysiology (Bethesda), (1997) Vol. 78, No. 1, pp. 51-62.
CODEN: JONEA4. ISSN: 0022-3077.
DT Article
LA English
ED Entered STN: 10 Sep 1997

Last Updated on STN: 10 Sep 1997
AB Capacitance measurements allow direct studies of exocytosis and endocytosis in single synaptic terminals isolated from bipolar neurons of goldfish retina. Extending the technique to intact bipolar cells, with their more complex morphology, requires **information** about the cells' electrotonic **architecture**. To this end, we developed a compartment model of bipolar neurons isolated from goldfish retina and tested the model experimentally. The isolated cells retained morphology similar to that of bipolar neurons in intact goldfish retina. In whole cell recordings, current relaxations in response to 10-mV hyperpolarizing voltage pulses decayed with a biexponential time course. This suggests that the cells may be described by a two-compartment equivalent circuit with compartments corresponding to the soma/dendrites (6-10 pF) and synaptic terminal (2-4 pF), linked by the axial resistance (30-60 M-OMEGA) of the axon. Four lines of evidence validate the equivalent circuit. 1) Similar estimates of somatic/dendritic and terminal capacitance were obtained whether the patch pipette was attached to the soma or to the synaptic terminal. 2) Estimates of the capacitance of the two compartments in intact cells were similar to estimates from somata and terminals that were isolated by cleavage of the connecting axon. 3) When current transients were generated from a more complete computer simulation of a bipolar neuron, analysis of the simulated transients with the use of the simple two-compartment model yielded capacitance estimates similar to those used to set up the simulation. 4) In isolated cells, the model gave estimates of depolarization-evoked increases in capacitance of the synaptic terminal that were quantitatively similar to those measured in terminals that were detached from the rest of the cell. Although in previous studies researchers have attempted to apply a similar equivalent circuit to more geometrically complex cells, morphological correlates of the equivalent-circuit compartments have been elusive. Our results demonstrate that in dissociated bipolar cells, precise morphological correlates can be assigned to the equivalent-circuit compartments. Additionally, the work shows that time-**resolved** capacitance measurements of synaptic transmitter release are possible in intact, isolated bipolar neurons and may also be feasible in intact tissue.

L7 ANSWER 44 OF 65 PASCAL COPYRIGHT 2009 INIST-CNRS. ALL RIGHTS
Full Text
RESERVED. on STN DUPLICATE 7
AN 1996-0319440 PASCAL

TIEN A distributed problem-solving approach to collaborative facility engineering
Computing in civil and structural engineering
AU KHEDRO T.
TOPPING Barry H. V. (ed.); KHAN Asad I. (ed.)
CS Center for Integrated Facility Engineering, Stanford University, Stanford, CA 94305, United States
Department of Mechanical & Chemical Engineering, Heriot-Watt University, Edinburgh, United Kingdom
SO Advances in engineering software : (1992), (1996), 25(2-3), 243-252, 20 refs.
ISSN: 0965-9978
DT Journal
BL Analytic
CY United Kingdom
LA English
AV INIST-18222, 354000043657800160
AB A framework for collaborative facility engineering is presented. The framework is based on a distributed problem-solving approach to collaborative facility engineering and employs an integration approach called Agent-Based Software Engineering as an implementation vehicle of this approach. The focal **entity** of this framework is a Multiagent Design Team (MDT) that comprises a collection of software agents (e.g. design software applications with a certain standard communication interface) and a design specialist, which together perform specific design tasks. Multiagent design teams are autonomous and form an organizational structure based on a federation **architecture**. Every multiagent design team surrenders its autonomy to a system program called facilitator, which coordinates the interaction among software agents in the federation **architecture**. Facilitators can be viewed as representatives of one or more teams that facilitate the exchange of

design **information** and knowledge in support of the design tasks they perform. In the federation **architecture**, design specialists collaborate by exchanging design **information** with others via their software agents, and by identifying and **resolving** design conflicts by negotiation. In addition to a discussion of the framework's primary components, its realization in an integrated distributed environment for collaborative building engineering is described.

L7 ANSWER 45 OF 65 PASCAL COPYRIGHT 2009 INIST-CNRS. ALL RIGHTS
Full Text
RESERVED. on STN DUPLICATE 8
AN 1995-0138495 PASCAL
CP Copyright © 1995 INIST-CNRS. All rights reserved.
TIEN Group data base design: addressing the view modeling problem
AU HAYNE S.; SUDHA RAM
CS Univ. Calgary, MIS, fac. business, Calgary AB, Canada
SO The Journal of systems and software, (1995), 28(2), 97-116, refs. 1 p.3/4
ISSN: 0164-1212 CODEN: JSSODM
DT Journal
BL Analytic
CY United States
LA English
AV INIST-18071, 354000059410010010
AB Today's organizations increasingly depend on the use of data base technology to manage their operations. Advances in technology have resulted in increasing the number and complexity of these data bases. Despite their growing complexity, all data bases have one thing in common: each must have gone through either a formal or an 'informal design process. Data bases must mirror reality accurately, and thus the design process must better capture that reality. The heart of the design process is the conceptual design, data model mapping, and physical design. Our research focuses on providing automated support for the first of these, e.g., conceptual design. Conceptual design is known to be a very difficult and time-consuming phase in the development of data base applications. This article describes the **architecture**, implementation, and use of a distributed graphical group data base design system. The group view modeling system (GVMS) is implemented in Microsoft Windows for networked personal computers. The main purpose of GVMS is to allow multiple designers (or users) to share conceptual design **information** in real time and **resolve** design conflicts through the electronic medium. The underlying data model, semantic data model, is extended to include distribution **information** as well as transactions and is represented as an extended **entity** relationship model. Diagram management techniques are implemented to aid in simplifying large complex designs. A small study demonstrated that groups of data base designers who define their view collectively outperform individuals

L7 ANSWER 46 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
Full Text
STN
AN 1994:177171 BIOSIS
DN PREV199497190171
TI Effect of genetic **architecture** on the power of human linkage studies to **resolve** the contribution of quantitative trait loci.
AU Eaves, Lindon J.
CS Dep. Human Genetics, Va. Commonwealth Univ., P.O. Box 3, Richmond, VA 23298-0003, USA
SO Heredity, (1994) Vol. 72, No. 2, pp. 175-192.
CODEN: HDTYAT. ISSN: 0018-067X.
DT Article
LA English
ED Entered STN: 26 Apr 1994
Last Updated on STN: 26 Apr 1994
AB The effect of genetic **architecture** (linkage relationships, dominance and two forms of non-allelic interaction) on the. power of marker studies to detect, locate and analyse the contributions of specific quantitative trait loci (QTLs) to continuous human traits is considered for randomly mating populations in linkage equilibrium under a two-locus model. The expected regression of the within-sibling-pair mean-square on number of alleles identical by descent (IBD) at two marker loci is explored for every possible pair of markers over a region of the genome containing two QTLs linked loosely (50 CM) or more tightly (20 CM). For the cases

examined, it is shown that epistasis between the pair of QTLs reduces considerably the total amount of **information** available for the location and analysis of the QTL effects. The overall effects of epistasis are more marked when there are duplicate gene interactions (i.e. genes operate in parallel) than when there are complementary interactions (i.e. genes operate in series). However, when there are complementary interactions, the regression approach is almost certain to fail to detect any evidence of epistasis. The numerical analysis suggests that methods of QTL analysis based on IBD in humans are unlikely to offer the **resolving** power that is desirable if QTLs are to be located precisely unless inheritance is very simple or prohibitively large numbers of highly selected individuals are available.

L7 ANSWER 47 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
Full Text
STN
AN 1993:389389 BIOSIS
DN PREV199396064689
TI Nesting biology and immature stages of the rophitine bees (Halictidae) with notes on the Cleptoparasite Biastes (Anthophoridae) (Hymenoptera: Apoidea).
AU Rozen, Jerome G. Jr.
CS Dep. Entomol., American Museum of Natural History, Central Park West at 79th St., New York, NY 10024, USA
SO American Museum Novitates, (1993) Vol. 0, No. 3066, pp. 1-28.
CODEN: AMUNAL. ISSN: 0003-0082.
DT Article
LA English
ED Entered STN: 23 Aug 1993
Last Updated on STN: 23 Aug 1993
AB **Information** on the nesting biology of the ground nesting Sphecodosoma dicksoni (Timberlake) and Conanthalictus conanthi (Cockerell) from the southwestern United States is added to previously published data to provide an understanding of nest **architecture**, cell construction, provisioning, egg deposition, laral feeding behavior, cocoon construction (in the case of S. dicksoni), larval defection, and voltinism of these species. No cleptoparasitic bees are associated with either species at present. Observations on nest provisioning and larval adaptations of the related Palearctic Rophites trispinosus Perez are included. Recovery of an intermediate-stage larva of Biastes emarginatus (Schenck) (Nomadinae: Biastini) from the nest establishes this host association of the cleptoparasite. Its larva and the mature larva of the related genus Neopasites are compared and are found to share many derived features. Based on **information** presented here and on published and unpublished accounts, a synopsis of the biology of the Rophitinae is presented based on 7 genera and 14 species. The synopsis identifies features that seem to be characteristic of the subfamily. The mature larvae of the Rophitinae are characterized on the basis of six genera, and a key to available species is presented. The mature larva of Sphecodosoma dicksoni and Conanthalictus conanthi are described taxonomically and compared with larvae of other Rophitinae. Also treated is an immature larva (probably last instar) of Rophites trispinosus. Whereas the mature larvae of S. dicksoni and R. trispinosus share many features with rophitine genera Dufourea and Xeralictus, that of C. conanthi is very different, though clearly sharing significant synapomorphies with the others. Many of its differences appear to be related to the fact that it does not spin a cocoon. The pupa of S. dicksoni is also described, the first such treatment for any member of the subfamily. New **information** on nesting biology and immatures of the rophitines, though supporting the monophyly of the subfamily, does not seem to demonstrate phylogenetic linkages with the Halictinae and Nomiinae or with the Andrenidae and Melittidae at this time. However, a number of characters are identified and discussed that may eventually be helpful in **resolving** these relationships.

L7 ANSWER 48 OF 65 DISSABS COPYRIGHT (C) 2009 ProQuest Information
Full Text
and Learning Company; All Rights Reserved on STN
AN 90:21219 DISSABS Order Number: AAR9105906
TI THE APPLICATION OF COMPUTER-SUPPORTED COLLABORATIVE WORK AND KNOWLEDGE-BASED TECHNOLOGY TO THE VIEW MODELING AND INTEGRATION PROBLEMS: A MULTI-USER VIEW INTEGRATION SYSTEM (MUVIS) (DATABASE)
AU HAYNE, STEPHEN CHARLES [PH.D.]; RAM, SUDHA [advisor]

CS THE UNIVERSITY OF ARIZONA (0009)
SO Dissertation Abstracts International, (1990) Vol. 51, No. 9A, p. 3125. Order No.: AAR9105906. 201 pages.
DT Dissertation
FS DAI
LA English
ED Entered STN: 19921118
Last Updated on STN: 19921118
AB This dissertation describes the **architecture**, development and implementation of a network application called MUVIS. MUVIS supports the design of distributed object-oriented databases by groups of potential users. MUVIS is a graphical system implemented on Microsoft Windows for personal computers attached to local area networks. It allows designers to share conceptual design objects in real-time and **resolve** naming conflicts through the electronic medium. It assists these database designers in representing their views and integrating these views into a global conceptual schema. The view integration component is decoupled from the view modeling component. The underlying data model, the Semantic Data Model (SDM), is extended to include distribution **information** and transaction specification. The visual interface to the SDM is an Extended **Entity** Relationship model, yet objects in the SDM are classes (as opposed to **entities** and relationships) and this fact reduces the complexity of the integration. An experiment involving groups of size three and four and individuals modeling a complex case validated the view modeling system. The groups were more efficient and produced higher quality designs than did individuals.

L7 ANSWER 49 OF 65 PASCAL COPYRIGHT 2009 INIST-CNRS. ALL RIGHTS
Full Text
RESERVED. on STN
AN 1991-0220479 PASCAL
TIEN Database of research structures in public and private institutions in the south of Italy
AU BIANCHI G.; BRANDI M. C.; SCARDA A. M.
CS CNR, ist. studi ric. documentazione sci., Rome 00185, Italy
SO Journal of information science, (1990), 16(5), 299-310, 10 refs.
ISSN: 0165-5515 CODEN: JISCDI
DT Journal
BL Analytic
CY Netherlands
LA English
AV INIST-14165, 354000015074750040
AB The methodology of a specific inquiry about the structure and the research activities of the institutions operating in the Mezzogiorno is presented. The project included setting up a conceptual schema which concerns structures, activities and ongoing research projects in public and private institutions. The need to choose a formal data model which will allow the correct execution of the design of the complex conceptual schema has been **resolved** by the adoption of the second generation formal model **Entity** Relationship. The main characteristics of the tool used to develop the database ADEPT (Application Design with **Entity** Relationship Programming Techniques) are explained

L7 ANSWER 50 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.
Full Text
on STN
AN 535031 RDISCLOSURE
TI Distributed system identification
PA Anonymous
PI RD 535031 20081110
PRAI RD 2008-535031 20081023
SO Research Disclosure, Vol. 535, 11 2008, p. 977
CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 6
GIS 46836; 51360; 58664; 72344; 53876; 62632

L7 ANSWER 51 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.
Full Text
on STN
AN 534003 RDISCLOSURE

TI Routing/forwarding **architecture** for pubsub networking
PA Anonymous
PI RD 534003 20081010
PRAI RD 2008-534003 20080902
SO Research Disclosure, Vol. 534, 10 2008, p. 829
CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 20
GIS 57694; 53420; 65352; 60800; 72640; 170904; 126254; 55344; 54096; 61298; 47090; 61634; 62178; 65700; 58754; 57348; 72872; 59942; 37026; 24120

L7 ANSWER 52 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.
Full Text
on STN
AN 511048 RDISCLOSURE
TI Possible enhancements to code-navigation tools and development environments
PA Anonymous
PI RD 511048 20061110
PRAI RD 2006-511048 20061020
SO Research Disclosure, Vol. 511, 11 2006, p. 1493
CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 8
GIS 73352; 56586; 550496; 67442; 43516; 38654; 55908; 58086

L7 ANSWER 53 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.
Full Text
on STN
AN 487006 RDISCLOSURE
TI Fault tolerant replication in a constellation of servers
PA Charles S. Johnson, Ronald M. Cassou, and Shang-Sheng Tung
PI RD 487006 20041110
PRAI RD 2004-487006 20041020
REN XP007134448
SO Research Disclosure, Vol. 487, 11 2004, p. 1403
CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 21
GIS 87432; 86792; 89748; 89828; 89772; 91550; 80506; 90184; 87032; 88508; 90202; 92876; 86148; 87538; 91298; 91784; 86584; 89972; 77470; 31756; 22058

L7 ANSWER 54 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.
Full Text
on STN
AN 466118 RDISCLOSURE
TI Method for referencing and managing arbitrary font technologies in a presentation environment
PA International Business Machines Corporation
PI RD 466118 20030210
PRAI RD 2003-466118 20030120
REN XP007132282
SO Research Disclosure, Vol. 466, 02 2003, p. 341
CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 2
GIS 47016; 21224

L7 ANSWER 55 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.
Full Text
on STN
AN 465205 RDISCLOSURE
TI Bluetooth hyper-scatternets vis web services
PA International Business Machines Corporation
PI RD 465205 20030110
PRAI RD 2002-465205 20021220
REN XP007132149

SO Research Disclosure, Vol. 465, 01 2003, p. 188
    CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 18
GIS 46978; 62168; 40328; 29418; 21182; 14792; 16482; 16364; 15750; 28028;
    98936; 41562; 58190; 48970; 44218; 47124; 44876; 9044

L7 ANSWER 56 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.
Full Text
    on STN
AN 462165 RDISCLOSURE
TI Implementing OpenSSL cryptographic functions using IBM's CCA program
    product
PA International Business Machines Corporation
PI RD 462165 20021010
PRAI RD 2002-462165 20020920
REN XP007131462
SO Research Disclosure, Vol. 462, 10 2002, p. 1939
    CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 2
GIS 49910; 45354

L7 ANSWER 57 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.
Full Text
    on STN
AN 446190 RDISCLOSURE
TI A generic input and output concept for message flows in MQSeries
    integrator V2 supporting physical segregation of organizational units
PA International Business Machines Corporation
PI RD 446190 20010610
PRAI RD 2001-446190 20010520
REN XP007128496
SO Research Disclosure, Vol. 446, 06 2001, p. 1079
    CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 10
GIS 26508; 53064; 34788; 139244; 41468; 39210; 31290; 18074; 39006; 13746
IPCI G06F
IPCR G06F0009-44 [I,A]; G06F0009-44 [I,C*]
EPC G06F0009-44G2G

L7 ANSWER 58 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.
Full Text
    on STN
AN 444187 RDISCLOSURE
TI Dynamically structured messaging mechanism
PA International Business Machines Corporation
PI RD 444187 20010410
PRAI RD 2001-444187 20010320
REN XP007128085
SO Research Disclosure, Vol. 444, 04 2001, p. 681
    CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 11
GIS 52548; 25514; 35386; 26852; 40084; 32022; 37478; 25528; 34478; 78508;
    17016

L7 ANSWER 59 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.
Full Text
    on STN
AN 439140 RDISCLOSURE
TI IBM standard software installer (ISSI)
PA International Business Machines Corporation
PI RD 439140 20001110
PRAI RD 2000-439140 20001020
REN XP001009395; XP007127181
SO Research Disclosure, Vol. 439, 11 2000, p. 2023

CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 8
GIS 37780; 136338; 46484; 49028; 33858; 48516; 42666; 23666
IPCI G06F
IPCR G06F0009-445 [I,A]; G06F0009-445 [I,C*]
EPC G06F0009-445N

L7 ANSWER 60 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.
Full Text
on STN
AN 430032 RDISCLOSURE
TI Algorithm for microprocessor frequency identification utility
PA Anonymous
PI RD 430032 20000210
PRAI RD 2000-430032 20000120
REN XP000969015; XP007125494
SO Research Disclosure, Vol. 430, 02 2000, p. 240
CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 4
GIS 39080; 58392; 11432; 18168
IPCI G06F
IPCR G06F0011-34 [I,A]; G06F0011-34 [I,C*]
EPC G06F0011-34C

=> d 61-65

L7 ANSWER 61 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.
Full Text
on STN
AN 426114 RDISCLOSURE
TI Multi-modal data access
PA International Business Machines Corporation
PI RD 426114 19991010
PRAI RD 1999-426114 19990920
REN XP007124971
SO Research Disclosure, Vol. 426, 10 1999, p. 1393
CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 8
GIS 45982; 41440; 53304; 52964; 49944; 52704; 20580; 14494

L7 ANSWER 62 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.
Full Text
on STN
AN 423111 RDISCLOSURE
TI Converting HTML to well formed XML with preference based tag expansion
PA International Business Machines Corporation
PI RD 423111 19990710
PRAI RD 1999-423111 19990620
REN XP007124645
SO Research Disclosure, Vol. 423, 07 1999, p. 1011
CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 3
GIS 47704; 43654; 43414

L7 ANSWER 63 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.
Full Text
on STN
AN 416150 RDISCLOSURE
TI Routine transaction management in a transaction service
PA International Business Machines Corporation
PI RD 416150 19981210
PRAI RD 1998-416150 19981120
REN XP007123738

SO Research Disclosure, Vol. 416, 12 1998, p. 1720
CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 4
GIS 51038; 28226; 35296; 39582

L7 ANSWER 64 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.
Full Text
on STN
AN 413047 RDISCLOSURE
TI The user destination model for networkscanning
PA Anonymous
PI RD 413047 19980910
PRAI RD 1998-413047 19980820
REN XP007123262
SO Research Disclosure, Vol. 413, 09 1998, p. 1194
CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 3
GIS 45908; 51282; 19018

L7 ANSWER 65 OF 65 GENBANK® COPYRIGHT 2009 on STN

LOCUS (LOC): CP000082 GenBank (R)
GenBank ACC. NO. (GBN): CP000082 AADI01000000 AADI01000001 AADI01000002
AADI01000003 AADI01000004 AADI01000005 AADI01000006
AADI01000007 AADI01000008
GenBank VERSION (VER): CP000082.1 GI:71037566
CAS REGISTRY NO. (RN): 925303-90-8
SEQUENCE LENGTH (SQL): 2650701
MOLECULE TYPE (CI): DNA; circular
DIVISION CODE (CI): Bacteria
DATE (DATE): 1 Nov 2007
DEFINITION (DEF): Psychrobacter arcticus 273-4, complete genome.
SOURCE: Psychrobacter arcticus 273-4
ORGANISM (ORGN): Psychrobacter arcticus 273-4
Bacteria; Proteobacteria; Gammaproteobacteria;
Pseudomonadales; Moraxellaceae; Psychrobacter
COMMENT:
URL -- http://www.jgi.doe.gov
Contacts: Paul Richardson (microbes@cuba.jgi-psf.org)
Hector L. Ayala-del-Rio (hlayala@hpcf.upr.edu)
Finished microbial genomes have been curated to close all gaps with
greater than 98% coverage of at least two independent clones. Each
base pair has a minimum q (quality) value of 30 and the total error
rate is less than one per 50000.
REFERENCE: 1 (bases 1 to 2650701)
AUTHOR (AU): Ayala-del-Rio,H.L.; Chain,P.; Ponder,M.A.; Di
Bartolo,G.; Ivanova,N.; Bergholz,P.W.; Hauser,L.;
Land,M.; Bakermans,C.; Rodrigues,D.; Klappenbach,J.A.;
Zarka,D.; Larimer,F.; Richardson,P.; Thomashow,M.F.;
Tiedje,J.M.
TITLE (TI): Complete sequence of Psychrobacter arcticum 273-4
JOURNAL (SO): Unpublished
REFERENCE: 2 (bases 1 to 2650701)
AUTHOR (AU): Copeland,A.; Lucas,S.; Lapidus,A.; Barry,K.; Detter,C.;
Glavina,T.; Hammon,N.; Israni,S.; Chain,P.; Di
Bartolo,G.; Ivanova,N.; Hauser,L.; Land,M.; Larimer,F.;
Pitluck,S.; Richardson,P.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (23-JUN-2005) US DOE Joint Genome Institute,
2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698,
USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..2650701	/organism="Psychrobacter arcticus 273-4"
		/mol-type="genomic DNA"
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                                     replication"
                                     /note="DnaA is an ATP- and
                                     DNA-binding protein. It binds
                                     specifically to 9 bp nucleotide
                                     repeats known as dnaA boxes which
                                     are found in the chromosome origin
                                     of replication (oriC).; Citation:
                                     Skarstad K and Boye E.  1994. The
                                     initiator protein DnaA: evolution,
                                     properties and function. Biochim
                                     Biophys Acta. 1217(2):111-30."
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                                     holoenzyme is responsible for most
                                     of the replicative synthesis in
                                     bacteria. The beta subunit is
                                     required for initiation of
                                     replication from an RNA primer."
                                     /note="A dimer of the beta subunit
                                     of DNA polymerase forms a ring
                                     which encircles duplex DNA.;
                                     Citation: Kong XP, Onrust R,
                                     O'Donnell M, Kuriyan J. 1992.
                                     Three-dimensional structure of the
                                     beta subunit of E. coli DNA
                                     polymerase III holoenzyme: a
                                     sliding DNA clamp. Cell.
                                     69:425-437."
                                     /codon_start=1
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                                     the interconversion of topological
                                     isomers of DNA and play a key role
                                     in DNA metabolism."
                                     /note="DNA gyrase is a type II
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                                     ATP-dependent 2 strand cleavage of
                                     DNA."
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                                     HKTLMLHSDQGWHYQMKPFREMLKKHQIKQSMSR
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gene                 complement(9413..9931)  /locus-tag="Psyc-0007"
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                                     CKHYGHSLRPSDIWTEIGKLVYYT
                                     AIGDFTCPRKYFFIAPLGVGTSLSDLLKNPRKLV
                                     QGLRENWDKYCKDKITQNCLIKLS
                                     DMEPQLEKIDFSIFGYVTPLTIIEQHRKTPHFIT
                                     RFGGGLPKREIPPEPPIKSTSEES
                                     EYLKKILQAYSDFNKQDISTIDDVTDIDLTEHYK
                                     DSRIQFYSAEALKRFSRDALPENE
                                     FKLLQQEFLNGIKDEIRNPVHANGYLRLLEVVKV
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                                     HQLANDNESIAWAKNG"
gene            complement(24177..24554 /locus_tag="Psyc_0021"
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CDS             complement(24177..24554 /locus_tag="Psyc_0021"
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                                        /note="This protein may be a
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                                        /translation="MVNNTDYVGTLFDNSESNLS
                                        KITLAFTMAGVALKKGHSASVILM
                                        VDAVYLALPNALDNVNIGAPFEPAGELLEAFIEK
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                                        FTVISGDDVVELLMNAKGSFQLN"
gene            complement(24825..25877 /locus_tag="Psyc_0022"
                )
CDS             complement(24825..25877 /locus_tag="Psyc_0022"
                )
                                        /note="This protein may contain an
                                        alpha/beta-hydrolase fold
                                        (COG0429) and an
                                        esterase/lipase/thioesterase
                                        active site (PS50187).  RBS
                                        found."
                                        /codon_start=1
                                        /transl_table=11
                                        /product="conserved hypothetical
                                        protein"
                                        /protein_id="AAZ17896.1"
                                        /db_xref="GI:71037588"
                                        /translation="MPTSKLTKPFSPAPFKPPFW
                                        LTNPHLQSILPKFFAPKTPNYRRV
                                        IKQDSLAETDIAYDFYDAYPVQHAENGALEQTPL
                                        IVLFHGMEGSSDSHYARALAYQIH
                                        AQGWHFVVAHFRSCGGIPANGKVFYNAGDTSEVH
                                        HMLENLRENYAHIYGVGVSLGGNA
                                        LAKYMGEYDDEALCDGAAVISAPVDMSSAAITMH
                                        SFLSHRIYTPYLLNPIIKKALANE
                                        ITADEIAAIKAVKRISDFDNIFTAPRHGYRSKND
                                        YYHSSSALPYLRNVTRPLLLISAK
                                        DDPFIGFTATPNDVSDSVTILDTAHGGHIGYLRY
                                        RADRSNVKTPSKKSKFDINWIPET
                                        VSAYFNHIGVPSNKTK"
gene            complement(26178..26774 /locus_tag="Psyc_0023"
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CDS             complement(26178..26774 /locus_tag="Psyc_0023"
                )
                                        /note="RBS found."
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                                        GGIKLGAGGLTRAYAGSAQAAVDEMTLSPYIPMV
                                        QAQILAEFATEAQCRYIVESLGGS
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                                        LESP"
gene            26978..27697            /locus_tag="Psyc_0024"
CDS             26978..27697            /locus_tag="Psyc_0024"
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                                        /product="ribosomal small subunit
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                                     /translation="MVGNRMRLDKFLSKATELSR
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                                     IAGRLDVDTTGALLISDDGGWLHRVTSPKHEHAK
                                     VYELTLADAMDSDAQANAIKEVAE
                                     GILLEGDHEETKPATLEFIDETHARLTLEQGKYH
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gene            28179..29264         /locus_tag="Psyc_0025"
CDS             28179..29264         /locus_tag="Psyc_0025"
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                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     1.000) with cleavage site
                                     probability 0.996 at residue 24"
                                     /codon_start=1
                                     /transl_table=11
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                                     /protein_id="AAZ17899.1"
                                     /db_xref="GI:71037591"
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                                     IVPSKLPNMYQVNLAEQLPLHITE
                                     DGKYVIQGELQKNPSKRVVTKTPARSTSAQIGKP
                                     VSASIKSDILANMGALKNMSAKTP
                                     FFYTAVPGVIWGATLEGVPFLLSDDAQYITDGEI
                                     SVIEKGQFTGLDSSFEKLKNQSVL
                                     TTLDTKQLITYPATSAEKAVIYVATDVNCPYCRR
                                     LHKQMSMLNAKGVTVKMIGYPIYE
                                     ESPEQMRGIWCQGNEDSRRKALDKAMLQGKMTPA
                                     PATCKTNDVAGNREKAAGLAVMAT
                                     PAIYREDGVLFQASFESPEFLEFLGVK"
gene            complement(29409..30059 /locus_tag="Psyc_0026"
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                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     0.935) with cleavage site
                                     probability 0.632 at residue 25"
CDS             complement(29409..30059 /locus_tag="Psyc_0026"
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                                     /transl_table=11
                                     /product="hypothetical protein"
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                                     /db_xref="GI:71037592"
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                                     KEAANGFIIQAVAGAITPQNIEKV
                                     INTQGQANTATKELAAAWAIASNQVDLKNLIQNL
                                     IIHRGDVNAVVKNQMQQIMEKQAD
                                     ELEKQAVQGTHSDKPKLSYCGINCFTISGQVKGY
                                     PLVIEMEREGLIDWKIIDIILP"
gene            30543..31667         /locus_tag="Psyc_0027"
CDS             30543..31667         /locus_tag="Psyc_0027"
                                     /function="chaperone activity"
                                     /codon_start=1
                                     /transl_table=11
                                     /product="probable chaperone
                                     protein dnaJ"
                                     /protein_id="AAZ17901.1"
                                     /db_xref="GI:71037593"
                                     /translation="MSKRDFYEILGVSKTADNKE
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                                     GQSRGGGGGRSRRGSDLRYVIELTLEEAVRGCKK
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                                     EISFTAPAPCDTCDGKGAKNASDI
                                     VTCQTCHGQGQVRMQQGFFAVQQACPHCGGTGKQ
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                                     PAGVDDGDRVRLSGEGEAGGAGVQNGDLYVEVRV
                                     KPHNVFTRQGADLYMDVPISITDA
                                     ALGKEVEIPTLDGKVKIKVAEGTQSGKLLRVRGR
                                     GVTPVRTTMKGDLICRVVIETPVN
                                     LTREQKDLLRQFQDTLDGDSKHQQSPHKKSFFKK
                                     IGDLFD"
gene                 31996..32832    /gene="dapB"
                                     /locus-tag="Psyc-0028"
CDS                  31996..32832    /gene="dapB"
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                                     /EC-number="1.3.1.26"
                                     /function="Diaminopimelate
                                     biosynthesis, Lysine biosynthesis
                                     via diaminopimellate"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="dihydrodipicolinate
                                     reductase"
                                     /protein-id="AAZ17902.1"
                                     /db-xref="GI:71037594"
                                     /translation="MSQQENKKMINVGVIGAGGR
                                     MGRMLIEAIQDNPQTALNAAIERQ
                                     GSSLVGADAGEVAAIGRLEVQIVDDLKAVINDID
                                     VLIDFSLPAATEQNMQVCAKHNVA
                                     MVIGTTGFNEQQEQVLAKASEQVAIVYAGNYSTG
                                     VNLSLKLLGMAAKAFGTDADVEII
                                     EAHHKHKIDAPSGTAYMMAEAVAEARGQNLKEVV
                                     VYGREGQTGAREAGTIGIHAIRGG
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gene                 complement(32915..34090
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                                     biosynthesis"
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                                     /protein-id="AAZ17903.1"
                                     /db-xref="GI:71037595"
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                                     EGRETPFLVVDLNRIKIKYHEMVG
                                     FFPNAKIHYAMKASPAVEVINLLAELGSNFDCAS
                                     IYELDRVLDCGVEASRISYGNTIK
                                     KPEHVKYAFDKGIDLYATDSEADLKNIAKHAPGS
                                     KIFVRILVQGSETAEWPLSRKFGC
                                     HPNMAIELLIQAQELGLVPYGISFHVGSQQKDVA
                                     AWDDALAKVKYMFDWMKNEEGIKL
                                     QMINLGGGFPANYLSEVNPIKVYAEEIKSYLSDD
                                     YSAEDMPEIILEPGRSLVGGSGVL
                                     VSDVVLISRKSHTDLTRWVYTDVGLFQGLIETLG
                                     EAIKYPVYTPKMETSTSAGTVVLA
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                                     AYTNSYSSIEFNGFPPLEVVYVN"
gene                 complement(34198..34752
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CDS                  complement(34198..34752
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                                     /locus-tag="Psyc-0030"
                                     /EC-number="3.5.1.88"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="peptide deformylase"
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                                     /db-xref="GI:71037596"
                                     /translation="MALLPILSYPDPRLRMIATP
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                                     IGLAASQVDHHIQLIVMDLSEDKDSPRVFINPKV
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                                     ERPNKVRIEAIDQNGNAIDEEVEGLLAVCIQHEI
                                     DHLNGVIFVDYLSRLKQTRARDKV
                                     RKVLKIREKQGEQVAEKEPQPANS"
gene            complement(35124..35378 /locus-tag="Psyc-0031"
                )
CDS             complement(35124..35378 /locus-tag="Psyc-0031"
                )
                                     /note="Signal peptide and 3
                                     transmembrane helices predicted.
                                     RBS found."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="conserved hypothetical
                                     protein"
                                     /protein-id="AAZ17905.1"
                                     /db-xref="GI:71037597"
                                     /translation="MSFIWMIIVGLVAGLLARAI
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                                     FVAGLIGINADGGFTGLIFSVIGAITLLFIYEMI
                                     MSKRRI"
gene            complement(35713..37230 /gene="mpl"
                )
                                     /locus-tag="Psyc-0032"
                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     0.973) with cleavage site
                                     probability 0.475 at residue 25"
CDS             complement(35713..37230 /gene="mpl"
                )
                                     /locus-tag="Psyc-0032"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="putative
                                     UDP-N-acetylmuramate:L-alanyl-gamm
                                     a-D-glutamyl-meso- diaminopimelate
                                     ligase"
                                     /protein-id="AAZ17906.1"
                                     /db-xref="GI:71037598"
                                     /translation="MHIHILGICGTFMGSLALLA
                                     RALGHTVTGSDANIYPPMSTQLEQ
                                     AGVTIEEGYLIAHLQPAPDLVVVGNAMKRGMDVI
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                                     RHVIAVAGTHGKTTTTTMLAWILHYAGIDAGFLI
                                     GGVPLVNTTDTNLQQVFAHSSYLG
                                     TEKDDSDNSVNTGYFVIEADEYDSAFFDKRSKFV
                                     HYRPRTAILNNLEFDHADIFADLD
                                     AIQTQFHHMVRMIPSTGKIIMPAATISLEDTLAK
                                     GVWTPIWRTSVIDSTISSVRREDS
                                     PLENSQAENSSDWQAELISADGSQFTVSFNDNKE
                                     ATALVNWSMSGLHNVNNALVAIAA
                                     AYNIGVSVKTACAALSAFAGIKRRMELIGDVNDI
                                     LVFDDFAHHPTAITTTLDGAKKKL
                                     ADRRLWAIIEPRSNTMKMGIHQDSLAQSATLADH
                                     TLWYEPTGLEWGLKEVIDNATIAN
                                     PSIGSQQVLSSVDDIIKHICTHAKAGDAIVIMSN
                                     GGFEGIHQRLLTALGNIVAIL"
gene            complement(37523..38146 /locus-tag="Psyc-0033"
                )
                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     0.963) with cleavage site
                                     probability 0.485 at residue 37"
CDS             complement(37523..38146 /locus-tag="Psyc-0033"
                )
                                     /codon-start=1
                                     /transl-table=11
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                                     /db-xref="GI:71037599"
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                                     QGAPINSDQSKVLNNDEAVLEENSAKASVNEDGR
                                     QEGQALIAAASSNDSSARSPMISA
                                     SNSDSILQATLMGDYGGVVPCPSCGSINITLNLF
                                     ADGSVLKTSVFNQAETPQPPLIES
                                     GVYRQDNDVITIVYEKKNIETYQIQNNHLIMMDE
                                     YKNPDEDYALARQ"
gene            complement(38341..38871 /gene="dsbB"
                )
                                     /locus-tag="Psyc-0034"
CDS             complement(38341..38871 /gene="dsbB"
                )
                                     /locus-tag="Psyc-0034"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="possible disulfide bond
                                     formation protein"
                                     /protein-id="AAZ17908.1"
                                     /db-xref="GI:71037600"
                                     /translation="MLQLTTYRNLQVFLVIMTAI
                                     GMSFALFFLQRYMGFSPCPLCIFQ
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                                     SCGPGLDYWLDTLPMQQVLKEVFAGSGECASIEW
                                     TFLGLSIPEQSLILFSILILTHLL
                                     ILWRIVRPSTPKPLAR"
gene            complement(38926..40509 /gene="gshA"
                )
                                     /locus-tag="Psyc-0035"
CDS             complement(38926..40509 /gene="gshA"
                )
                                     /locus-tag="Psyc-0035"
                                     /EC-number="6.3.2.2"
                                     /function="First step of the
                                     glutathione biosynthesis pathway"
                                     /codon-start=1
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                                     /product="glutamate-cysteine
                                     ligase"
                                     /protein-id="AAZ17909.1"
                                     /db-xref="GI:71037601"
                                     /translation="MILMSNFASSFVDFDIPNWF
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                                     KSSPKETLTMLRQLHLLVYQGMPE
                                     DELMWPLSMPCMLSSNDEDIPLADYGSSNTGKLK
                                     TLYRSGLGVRYGRRMQTIAGLHYN
                                     LSFGDNLFTAWQAQTPTAQAMTLTEFKNDKYLGL
                                     IRNFKRLTSLVLYLLGASPSVCPC
                                     FVSGIEHDLELFNNSTYYKPTATSLRMGKLGYTN
                                     SVQEHLDIRYNNLPEYIKGLRRAI
                                     QTPHESFEKLGLDDENGNPIQINNHILQIENEYY
                                     SPIRPKQIAMSGESPTEALERRGI
                                     AYVEFRAIDLDPYSDIGIRLSSACFLEVMALYCL
                                     LSDSPELMPEEEEALAINIERVVN
                                     EGRRENLQILNNGVEQSLESWMLMHLNRMQPLAA
                                     LLDAHYGGNDYRAAVALMQGKAGH
                                     SESTISAQVNSDSKRLGSLWQLGFTLAQQHRESL
                                     LQQTLSPNTQAKYEVLAEKSILQQ
                                     AEMEEAETEDFMNFLQQYR"
gene            complement(40901..41281 /locus-tag="Psyc-0036"
                )
CDS             complement(40901..41281 /locus-tag="Psyc-0036"
                )
                                     /note="Protein of unknown
                                     function, HesB/YadR/YfhF family.
                                     RBS found."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="conserved hypothetical
                                     protein"
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                                     /protein-id="AAZ17910.1"
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                                     LNLTDSAAQKVRRLREEEGDSNLM
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                                     VTLVVDSLSYQYLQGSTVDYTEGL
                                     EGARFIVTNPNATTTCGCGSSFSI"
gene            41787..43805         /locus-tag="Psyc-0037"
CDS             41787..43805         /locus-tag="Psyc-0037"
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                                     /transl-table=11
                                     /product="ABC transporter related
                                     protein, fused ATPase domains"
                                     /protein-id="AAZ17911.1"
                                     /db-xref="GI:71037603"
                                     /translation="MIEFKDVGVRRDGRELFAGA
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                                     ATLNDLSSVSDEQIGVLHQQFDEIDGYRTPTKAA
                                     QIMAGLGFNTNQHELPVEGFSGGW
                                     RMRLNLAKTLMSRADLMLLDEPTNHLDLDAILWL
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                                     VGHILHVEQQKITLYTGNYQQFIRTRHERMAQQQ
                                     QAFEKQEATKAHLDDFIRRFRAKA
                                     SKAKQAQSRIKQLERMAELSPMMADNPFSFRFYE
                                     PANMSSPLIELTDADIGYSDTPLL
                                     YNANVQVTPDTRIGLLGMNGAGKSTLIKALVGEL
                                     GVLTGSYNVSDTLKLGYFNQHQMD
                                     ILDPKATPIEMLRRLAGKTSDAMLRSFLGSFDFR
                                     GDRIDTISELFSGGERARLTLALI
                                     VWQRPNVLVLDEPTNHLDLQMRQALTIALQGFEG
                                     AVVLVSHDRELIANVCDELFLVHD
                                     GQIDEFDGDISDYGKWLAEKRKQENSQDKNTSKK
                                     KSKKESKKFVSRETNANSAGSQAG
                                     KQVGNSESQPALSKDAQRKLAAEQRKLTAPIRRD
                                     IETTEKTLATIDEKLLVLEEKLAN
                                     TDLYEESRKADLMTLLNEQTMLQQQHSQHEEKLL
                                     LAMTTLEEMEASIG"
gene            complement(43911..44279 /gene="rlpA"
                )
                                     /locus-tag="Psyc-0038"
                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     1.000) with cleavage site
                                     probability 0.999 at residue 23"
CDS             complement(43911..44279 /gene="rlpA"
                )
                                     /locus-tag="Psyc-0038"
                                     /function="prc mutant suppressor"
                                     /note="Lipoprotein conserved
                                     domain"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="putative lipoprotein A"
                                     /protein-id="AAZ17912.1"
                                     /db-xref="GI:71037604"
                                     /translation="MSYLIKSLVITLSILLSATA
                                     FAHNTNTSYYGSKFHGKRTASGSI
                                     FNMNSLTAAHRTLPFGTKVQVTNKKTKQSVIVKI
                                     TDRGPFIRGRILDLSKAAAGQINC
                                     QLCTTTMEILSYGDGRYRRE"
gene            44824..45822         /locus-tag="Psyc-0039"
CDS             44824..45822         /locus-tag="Psyc-0039"
                                     /function="DnaJ is a chaperone
                                     associated with the Hsp70
                                     heat-shock system involved in
                                     protein folding and renaturation
                                     after stress."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="probable heat shock
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                                     GDGEAYGDGGFRFDDIFSAFGRGARGQTNGQAGG
                                     QSQYGGFGSQDSKGQDQHAEITVD
                                     LASVYNGDDYSIKLNVPIRQPNGSVDYDNKTLKI
                                     KIPKGITDGKQIRLAGQGAAGSGS
                                     GKNGDLFLKVKLSHAANIRIEGADVYQTVNIAPW
                                     EAALGEKINVSTPAGTLGVTIPKN
                                     SKSGSNLRLKGKGIPAKQAGDLYLTLNIVNPHIN
                                     SEAATNAYEALKQAFADTTIER"
gene            45908..46231         /locus_tag="Psyc_0040"
CDS             45908..46231         /locus_tag="Psyc_0040"
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                                     /translation="MKHSPEFNDIIMSLDELISA
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                                     EQFTGYQLTTVRRASRLSRDFEASVPAIGLILEL
                                     LAEVEQLRQLKRQLDMQAPVIEIN IEHLK"
gene            complement(46320..47522
                )                    /gene="sstT"
                                     /locus_tag="Psyc_0041"
CDS             complement(46320..47522
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                                     /locus_tag="Psyc_0041"
                                     /codon_start=1
                                     /transl_table=11
                                     /product="serine/threonine:Na+
                                     symporter, SstT"
                                     /protein_id="AAZ17915.1"
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                                     LVLGVLIGWLAPNIGIALGLLGTL
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                                     TELVLVNAVIEPVPPANLKEVLTNLLMNLVANPV
                                     NAIAEANYIGILAWAIIIGFSLRQ
                                     ASDTARTVVGDFSDAISQVVKWVIALAPFGILGL
                                     VANTVAETGFAALAGYARILMVLV
                                     GCMLFIALVVNPLIILVKTGKNPYPLVFICLRES
                                     GITAFFTRSSAANIPINMNLARKL
                                     GLHEDTYSVTIPLGATINMAGAAITINVLTLAAA
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                                     FIIGVIQDSAETALNSSTDVLFTA AADPKYAR"
gene            complement(47861..48319
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CDS             complement(47861..48319
                )                    /gene="holC"
                                     /locus_tag="Psyc_0042"
                                     /EC_number="2.7.7.7"
                                     /function="The DNA polymerase III
                                     holoenzyme is the polymerase
                                     responsible for the replication of
                                     the chromosome."
                                     /note="Chi forms a 1:1 heterodimer
                                     with psi.  The chi:psi complex
                                     functions by increasing the
                                     affinity of tau and gamma for
                                     delta.delta allowing a functional
                                     clamp-loading complex to form at
                                     physiological subunit
                                     concentrations."
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                                     subunit"
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                                     LLSALNEALWTQEATSFIPHQYLLDADTDINHKT
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                                     PVNTFMAATNNAQPTRVLELIKPDATSVQEGRHK
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gene            complement(48355..50013  /gene="pepA"
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                                     /locus-tag="Psyc-0043"
CDS             complement(48355..50013  /gene="pepA"
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                                     /locus-tag="Psyc-0043"
                                     /function="Polypeptide
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                                     /product="PepA aminopeptidase.
                                     Metallo peptidase. MEROPS family
                                     M17"
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                                     /db-xref="GI:71037609"
                                     /translation="MNIKLTQSLPKTHTQKILKK
                                     EAKSKDAACLVVLIDDKKNILAES
                                     VLSDYQTRIEQLIEVSHFNGKACETVADYALAGD
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                                     SVLQKIANTIYKSTQKRVDSITVALGDTLEENQF
                                     GQFALNLLAASYRFDKYKSEQQTP
                                     VLTDIYLLADPSLEDSLNFAQAVFAGQSLTRDVA
                                     NEPGNICFPAYMAEQAQELAATYP
                                     NLLKVTVLGEKEMSALGMNCFLAVAQGSTKEGKL
                                     VLMEYRGQSNFSATADTSKATTNS
                                     AKVAGGLKALADKLPSKKAAKKADQNSEDNAHAA
                                     NNDAPIVLVGKGVTFDSGGISIKP
                                     GAAMDEMKFDMGGSAAVLGTIKALCEARLPINVV
                                     GALACAENMPSGDATRPGDIIRAM
                                     NGKSVEILNTDAEGRLVLCDTLCYVQRYQPKAII
                                     DVATLTGACVVALGHVRSAVFSND
                                     EDVLFDLENASHLSGDLIWHMPMDDEYQAQLDSP
                                     IADMQNIGGKGAGAVTAACFLSRF
                                     VEEGQAWAHLDIAGTAWISGQDKAATGRPVPLFM
                                     QYLKNSANMA"
gene            complement(50261..50866  /locus-tag="Psyc-0044"
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CDS             complement(50261..50866  /locus-tag="Psyc-0044"
                )
                                     /EC-number="3.3.2.1"
                                     /function="Ubiquinone synthesis"
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                                     /product="probable isochorismatase
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                                     /protein-id="AAZ17918.1"
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                                     /translation="MSIPSTLLGLSGGQFNEIDW
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                                     IKMHPNAFYDTELQALITSAGKQQIIFAGFMSHM
                                     CVSSSVRAAFDLGFESFVCHDACA
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gene            51384..52634         /locus-tag="Psyc-0045"
CDS             51384..52634         /locus-tag="Psyc-0045"
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                                     SSENVWQQQALTSAFDLIRPNQFISSGNYHLYVG
                                     SLSDDKKQLQDVILIQSEPEKKGS
                                     AVKNNTAKTNTAKNSAMDVENNIDPETAEQLNIP
                                     ELPNALANSTNISKDAITLAKRAQ
                                     QVDTGNSGVTQLDLFQGRRYEVGAGSLKYNQVGF
                                     DRYRITLTESSKEVITEDNIETQA
                                     IGPLWQAATGNAQVGSNNAMRAAQGELGYRLSLP
                                     WLMIIAPMLAVPLAQVRPRQGRWL
                                     RLFPSILLFVSCVLGIISLKNAVGKGSVSVWAYA
                                     WLILGFMALALYINWGSRVQHRLR
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gene            52634..53842         /locus-tag="Psyc-0046"
CDS             52634..53842         /locus-tag="Psyc-0046"
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                                     SELVVMRAAGISVYRIVSWVLQPALIFVVLALII
                                     NQFVLPHSNQLANEINSKGNSSLV
                                     TSVRGYWTVQPRFENTKRGTTKPDGSDILYIDYA
                                     DVKGNIGQVKRWHLDNNGSLQTAI
                                     HAEGGQYIGREPLDTVSSKPSEQYRYEWQLNNMT
                                     KLMINQGFESSQAISPTDTLSLPF
                                     APESVYLLTHQAEDLSLTQLYEHRQFMRQQGQRS
                                     LSHELAFWQKLLSPLSILSLVIVA
                                     CSFVFGSLRTHSLGLRIVVALLFGLLFSYVQDLV
                                     GFVSLATGFSPLLMVLLPIIASAL
                                     LGEYLLKRQM"
gene            complement(53920..54528 /locus-tag="Psyc-0047"
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CDS             complement(53920..54528 /locus-tag="Psyc-0047"
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                                     /note="Possible 16S RNA G1207
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                                     ARECPNGQHTLIDKDFMAVEYARL
                                     NCEKNGLNNVDVHLSNGFNHVDKAKDFSLVMSNL
                                     PAKVGKEQHYLYFLDAHARMRKGG
                                     RFYVVTINGLRQFMKRSFIEVFGNSEKVKQGKTY
                                     TITMATKD"
gene            complement(55288..55752 /locus-tag="Psyc-0048"
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                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     0.998) with cleavage site
                                     probability 0.955 at residue 22"
CDS             complement(55288..55752 /locus-tag="Psyc-0048"
                )
                                     /note="Signal peptide and 5
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                                     /protein-id="AAZ17922.1"
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                                     AVVTALLILFFEPNHTVTLMDVPKWQLLGALCGV
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                                     GQLSMSVLIDNFGLLGNEAISLSGSRISALVCLA
                                     IALYFIYASSNSEPKEAQ"
gene            complement(55758..56192  /locus-tag="Psyc-0049"
                )
                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     0.939) with cleavage site
                                     probability 0.836 at residue 21"
CDS             complement(55758..56192  /locus-tag="Psyc-0049"
                )
                                     /note="Signal peptide and 5
                                     transmembrane helices predicted.
                                     RBS found."
                                     /codon-start=1
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                                     /protein-id="AAZ17923.1"
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                                     ALTFFLMLFFSPRDSPSFFSQPPLLLVGGILGPV
                                     YVVVLTVVTPVIGIALTMIGILAG
                                     QVFQSLIIDHYGLFETMERKIDSKRIIALFFIIA
                                     ALFFMAKG"
gene            56291..57226         /locus-tag="Psyc-0050"
CDS             56291..57226         /locus-tag="Psyc-0050"
                                     /function="The majority of these
                                     proteins appear to be
                                     transcription activators and most
                                     are known to negatively regulate
                                     their own expression. All possess
                                     a potential HTH DNA-binding motif
                                     towards their N-termini."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="transcriptional
                                     regulator, LysR family"
                                     /protein-id="AAZ17924.1"
                                     /db-xref="GI:71037616"
                                     /translation="MNTVDTINIQTLLFFIEVFD
                                     AQSFSVVARKEGVSASKVSRIIRQ
                                     LEDSLGQQLFYRNTRAVTPTEAGRVFMRYAKSMT
                                     ESMSAAQQELQDRTLEPGGLIRIN
                                     APVFFGQRHIAPWLPQLSAQYPKLQIDLSLTDDF
                                     IDPHHYATDVIFRIGTLNDSAFHA
                                     RIFGEQTYHLAASPSYISTHGKLQVPADLTHHKC
                                     LLYKGSTGPNRWLFKTESEDWTPF
                                     LAPALLMSNNAESLLVSALKGMGIVLFPDWLIGE
                                     HLKSGELIKLLPNYSTAVKTTPQH
                                     VAAIYPHTRHVSLNVRALIDYFAKVYGHPLYWQL
                                     N"
gene            57548..59107         /locus-tag="Psyc-0051"
CDS             57548..59107         /locus-tag="Psyc-0051"
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                                     /transl-table=11
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                                     MVTSSPEHIIKNARWRINDNLAGT
                                     RHFCPMLVKTEAFTQAAALDIATMVEKLNDEFGQ
                                     DLLMRASVWMTLRESKASFTIEGE
                                     GKELKRIERFAEVMARRTGKGDIPLDPESLAELQ
                                     QEILGSKTVIQQYGIRQSPVFVSH
                                     TQVNGFKEIVHYIAPPSEDIAYKLTGLQALMKKT
                                     EGQSALMRSAVASFAFVYIHPLAD
                                     GNGRVHRFLINDVLRRDQVIHEPIILPISQAIAE
                                     HPSDRHAYDKILDRVSVPLMRQIR
                                     DHYRFDKQAVTYPDGIRSNLNFADSHLIQPAWRF
                                     MDLTPHVQYLSGLIAHVIEKEMHN
                                     ESQYLRQHDHARLAIKEIVEMPNSYADRIIRSML
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gene            complement(59255..60193
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CDS             complement(59255..60193
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                                     /locus_tag="Psyc_0052"
                                     /function="Members of this family
                                     cleave DNA substrates by a series
                                     of staggered cuts, during which
                                     the protein becomes covalently
                                     linked to the DNA through a
                                     catalytic tyrosine residue at the
                                     carboxy end of the alignment."
                                     /codon_start=1
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                                     integrase"
                                     /protein_id="AAZ17926.1"
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                                     /translation="MSRDRAVQQRQPKALAVDDE
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                                     KTPRTQARMLSSLRQFYLWMIASN
                                     LREDNPCERIKSPKLGRPLPKDLAEADVDNLLAA
                                     PDSSTALGLRDKAMLEVLYACGLR
                                     VSELVNLSLEQVNLNSGWLQITGKGNKTRLVPLG
                                     EYASDALEDYLTHGRGDLIAHLKA
                                     GNCQAVFLTAQGGYMTRQNFWYLLKKYAKVASID
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                                     SVQLLLGHSNLSTTQIYTHVATARLQKLHAEHHP
                                     RG"
gene            complement(60448..61662
                )                    /locus_tag="Psyc_0053"
CDS             complement(60448..61662
                )                    /locus_tag="Psyc_0053"
                                     /note="This protein contains a SAM
                                     (and some other nucleotide)
                                     binding motif.  RBS found."
                                     /codon_start=1
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                                     TNERSEQRKINKAANKSAKSGKPT
                                     DEASVTSKVIPNLFHQQRQTQSQRSRLLSRLLLE
                                     LDAGYVSQLRRAPDVSAACTAAFG
                                     ELNESCLLSFRDLQGALGAAGWRVKGVAIENLGL
                                     SIFPHYGVFAPTRHEYVQLLLDAP
                                     LPAVYDVAFDIGTGTGLLAIILAQRGVKQVIATD
                                     LNPRALACASENLARLELPAVQLQ
                                     QADLYPTDAPLANLLVCNPPWLPAKPTSPLEFAV
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                                     YDANSTMLRGFLQSAKQHLAEHGE
                                     VWLILSDLAEHLQLRSRDELLSWFANAGLEVKYR
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                                     ITSLWCLVPFNT"
gene            complement(61869..62129 /locus-tag="Psyc-0054"
                )
CDS             complement(61869..62129 /locus-tag="Psyc-0054"
                )
                                     /note="Possible redox protein
                                     regulator of disulfide bond
                                     formation, Sir A.  RBS found."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="conserved hypothetical
                                     protein"
                                     /protein-id="AAZ17928.1"
                                     /db-xref="GI:71037620"
                                     /translation="MTTSTLDSNINHHLDTQGLI
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                                     ATDPATTRDIPNFCRHLGHTLVRQEILNDAPTYR
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CDS             complement(62205..62717 /locus-tag="Psyc-0055"
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                                     /product="hypothetical protein"
                                     /protein-id="AAZ17929.1"
                                     /db-xref="GI:71037621"
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                                     TIPLTLYNAFIIYRYRLNQTSMVI
                                     MTIGVSSIILIGGLLFADTAWLGLASWLGVAFLF
                                     KVSFKRFFNFLALADLPENNKSAE
                                     NNETITTTDA"
gene            complement(62796..63329 /locus-tag="Psyc-0056"
                )
CDS             complement(62796..63329 /locus-tag="Psyc-0056"
                )
                                     /note="This protein contains a
                                     ribonuclease RNase H fold
                                     (COG0816).  RBS found."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="conserved hypothetical
                                     protein"
                                     /protein-id="AAZ17930.1"
                                     /db-xref="GI:71037622"
                                     /translation="MVDSTLIKDSNDTDTDTGVA
                                     EPAIKPHLILALDYGVKKMGMALG
                                     NSLTETARAFDILAMNNGQPDWDNLLGIIKVWGV
                                     AKVVVGLPLNMDGSSSMLSKRAHK
                                     FARRLAHRIMEQHLPVIVSLCDERLTSVAAREIA
                                     WENGWIQNERDPIDDISACILMST
                                     YFADPNSSIAIDAIKAD"
gene            complement(63380..63943 /gene="algH"
                )
                                     /locus-tag="Psyc-0057"
CDS             complement(63380..63943 /gene="algH"
                )
                                     /locus-tag="Psyc-0057"
                                     /note="contains putative DNA
                                     binding region also has domain hit
                                     to protein DUF 179"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="putative transcriptional
                                     regulator"
                                     /protein-id="AAZ17931.1"
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                                     /translation="MSKANLTHHFLIAAPELSDP
                                     RFEQALIYICRHDKHGALGLMINR
                                     PLEQSRVGKLLEDLDIEVTDAQVMEDLALEGGPM
                                     YPEVGFVLHTGQPEWASSFAISEN
                                     VCITTSQDILKRIAAGQGVGHYQLCLGHASWGKK
                                     QLDQELANGDWLVCPADLNLLFDT
                                     PFEERWQIAADKIGVNFDYLSSDIGHA"
gene            complement(64062..65741 /gene="recN"
                )
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CDS             complement(64062..65741 /gene="recN"
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                                     /locus-tag="Psyc-0058"
                                     /function="All proteins in this
                                     family (TIGR00634) for which
                                     functions are known are ATP
                                     binding proteins involved in the
                                     initiation of recombination and
                                     recombinational repair."
                                     /codon-start=1
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                                     protein"
                                     /protein-id="AAZ17932.1"
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                                     RSKAWLNGTPVSLAELKSLGSLLVNIHSQHAQQA
                                     LLKPQFVVQWLDEMAQITSLTTKT
                                     TSSYQQYQQLKRRADDLASREAQRQDRIQLLQSQ
                                     LADIAPLLVVDYAEVEAEHEELSN
                                     IEALMIEASHGLHLLDNDTDEPDVMTLLGQAIKL
                                     CDNQMSVSQTFEQASEQLHLAQQQ
                                     ITEVTSLLSDYAEQQLPDPERLQSLDSLISLGHR
                                     LSRKHNLPANDLINEAKGWEAQLE
                                     QLENEPSSDAMAVQIEQAWQEYIALATELNKERS
                                     KAAPIVSKQLIKQLQPLALPNARC
                                     EFVFTKKTDVSQYNGQGCYDIDLLFSANVGMPMQ
                                     PLHKIASGGELSRMALVMQVLQAT
                                     NADNNAAKPMLVFDEVDVGISGGTAQVVGELLRA
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                                     ITDVTRDHARSLLSDVK"
gene            66427..66762         /locus-tag="Psyc-0059"
CDS             66427..66762         /locus-tag="Psyc-0059"
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                                     /db-xref="GI:71037625"
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                                     VQYICHLEG"
gene            66968..67738         /locus-tag="Psyc-0060"
CDS             66968..67738         /locus-tag="Psyc-0060"
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                                     /transl-table=11
                                     /product="probable RNA
                                     methyltransferase, TrmH family,
                                     group 3"
                                     /protein-id="AAZ17934.1"
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                                     /translation="MAKPTYFYGIHAIDALLEYR
                                     PLDGLSLFVQQGRETDSHVQAIMA
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                                     AIIMGSEGEGMRRLTTESCDELVY
                                     IPMSGNEHGNLQSLNVSVATGMALYEINRQRTLA
                                     AGQA"
gene            complement(67701..68393 /gene="coaE"
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CDS             complement(67701..68393 /gene="coaE"
                )
                                     /locus-tag="Psyc-0061"
                                     /EC-number="2.7.1.24"
                                     /function="Biosynthesis of
                                     pantothenate and CoA"
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                                     /product="Dephospho-CoA kinase"
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                                     AQQGIDIIDADVIAHEVVVKGSATLRKIQRKFGD
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                                     LIELEAITHPAIREAAKLQLAESTSPYVVLSAPL
                                     LIEAAEAGLANLCQRILVMDATED
                                     TQLARASQRDALSVQKIKAIMVNQLSREERNLHA
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                                     LKLAQQLKFAAD"
gene            complement(68477..69376 /gene="pilD"
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CDS             complement(68477..69376 /gene="pilD"
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                                     activity"
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                                     peptidase 1. Aspartic peptidase.
                                     MEROPS family A24A"
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                                     RQECSQFMYEQADIPREHTTPLVNIIATDIPITL
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                                     WIVLRGRCSECKTTIGLRYPVVELVTALLSVLVI
                                     YQFGVSTAGLSALILVWTLVVLTG
                                     IDFDTQLLPDRLTFPLAGLGLAVNSQGWFVSPTQ
                                     SIWGLLLGFLSLWIVVKIFYLITK
                                     KHGMGQGDFKLLAVLGAWLGPVMLPLVILLSSLL
                                     GSIVGLILIKKQGESKPFAFGPYI
                                     AIAGIVALLYGSDIVNWYLGMYN"
gene            complement(69402..70625 /gene="pilC"
                )
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CDS             complement(69402..70625 /gene="pilC"
                )
                                     /locus-tag="Psyc-0063"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="pilin secretion/fimbrial
                                     assembly system protein, PilC"
                                     /protein-id="AAZ17937.1"
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                                     /translation="MAKAKTDMLLDFVYDGVNRR
                                     GQKVKGETTSHSLELAKATLRKQG
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                                     KDLVLQIKADIEAGGNFASALRRHPRYFDDLFCS
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                                     PMID: 12711396 [PubMed - indexed
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                                     Mol. Biol. 2003 Mar
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CDS             97383..98273         /locus-tag="Psyc-0085"
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                                     fructose-1,6-bisphosphate into
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                                     glyceraldehyde 3-phosphate."
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                                     KASILRHLERLNDEQQVILKLTLP
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                                        IDICLPAVGQGALAIECRADDDEV
                                        LKLLAPLNDDKARIRLIAERALNRHLQGGCQVPI
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gene            104539..105522          /gene="hemD"
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                                        QYQQWLQDFDSQNAIGGITISQQAKPIVIVSSGT
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gene            complement(107401..1085 /gene="ribB"
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                                     AVSSNRGLVVPVLRDTDRMSMADVEAKIREFGGK
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                                     GSLMSTPILNPPQTAILGMHAINDRPMAVNGEVK
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CDS             123590..125041       /gene="lpdG"
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                                     CKTNLDGVYAIGDLVRGPMLAHKA
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                                     WVGLTEQEAEAAGYEVKTGSFNLA
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gene            125228..126394       /locus-tag="Psyc-0105"
CDS             125228..126394       /locus-tag="Psyc-0105"
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                                     YPVQTELYLGAVVDRSSRRVTFMASTEGGVEIEK
                                     VAEETPEKIFKVSIDPLVGLLPFQ
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                                     YVALEGNIGCMVNGAGLAMATMDI
                                     IKLYGGKPANFLDVGGGATKDRVVEAFKIILEDS
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                                     LFQEDPQTEAIILIGEIGGTAEEE
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                                     DPSKLGEKLKEVTGW"
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CDS             127483..128514       /gene="galE"
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                                     LEDLAASDKSWSLIPLRYFNPVGAHSSGSIGEDP
                                     NDIPNNLMPYISQVAVGKLDKLSI
                                     FGNDYATVDGTGVRDFIHVTDLAEGHVAALNYLK
                                     QQPQSLGFLPINLGTGKGTSVLEL
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CDS             128569..129453       /gene="galU"
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                                     PFNGDMSADNLAFMMDAFAKDNHS
                                     QILVDKVADEDVHKYGIAQLNEALSGVSSVDNEI
                                     DANISFKVAGFVEKPNVVDAPSRL
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CDS             129457..131124       /gene="pgi"
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                                     DTLSNAKTALSWLLATAKLRAGTEDSVRRRHFIG
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                                     DDHFAQADFAKNVPVLLGLIAVWN
                                     STFLQVNAHTVLPYDGRLSYLPSYLTQLEMESNG
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                                     TPLQQQHELSLANCLAQSRVLAFG
                                     NAAIAESDGQVACDADKYKYYRGNQPSTTLLLDE
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                                     DINPFDQWGVEMGKQMAESVHDAMQQERGAQFDT
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gene            131165..132595       /locus-tag="Psyc-0110"
CDS             131165..132595       /locus-tag="Psyc-0110"
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                                     ETANHNNSLFTNESQEINESQEINEPKTVALYWL
                                     FLDSIDSVWIEDDWLTAFNHSHQQ
                                     AQPLMMSGIKQLGTIAALSQRLKRAWVYYLPFVF
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                                     SRHHLGMLQPLMQHARATHYADIATIEFARSSIM
                                     AMLATRVSFMNEMSRLADSQKVDI
                                     QQVSHIMGLDERVGNSYLQAGWGFGGHTLPAELL
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gene            complement(132855..1343 /gene="cpsG"
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                                        LGMTGTEEVYFATSHYQALGGIEVTASHNPINYN
                                        GLKLVKEHSKPISADDGLAEIQAL
                                        AESGQFTADNALGKLQLLTDKSAYINHVMTFVDI
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                                        IDKLMQAGAPIEVITLHHTPDSSFPNGIPNPMIE
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                                        FDRCFLFDEYGDFIDGSYIVGMLAQAFLNKYPAE
                                        SIVYDPRVIYNTEAVIHEHNGNAV
                                        ISKSGHSFIKQVMRDSGAVYGGEMSAHHYFRDFF
                                        YCDSGMIPWLLTIELLSITGKTLS
                                        ALVSGYIKAYPSSGELNFRLTTHDAPTIISAIEV
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CDS             134490..135356          /locus-tag="Psyc-0112"
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                                        /protein-id="AAZ17986.1"
                                        /db-xref="GI:71037678"
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                                        TTLQEKLIRRHPHVFEAEILADDAAVKVRWDEIK
                                        IEEEQTRAVRGKPKRRLDNTKAGS
                                        ALMQAQEVQKQASKLGFDWEGISGAFDKLDEEVN
                                        ELKAEIVNKTKEEIKEKITDIEKE
                                        LGDCMFALVNVARKLNLDAETATLTCIHKFKSRF
                                        GYIEEQLAAAGKRLEDSDINEMDA
                                        LWEAAKLHERTQ"
gene            135367..135714          /gene="comEA"
                                        /locus-tag="Psyc-0113"
CDS             135367..135714          /gene="comEA"
                                        /locus-tag="Psyc-0113"
                                        /note="Signal predicted by SignalP
                                        2.0 HMM (Signal peptide probabilty
                                        0.995) with cleavage site
                                        probability 0.936 at residue 24"
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                                        /transl-table=11
                                        /product="putative competence DNA
                                        binding protein ComEA"
                                        /protein-id="AAZ17987.1"
                                        /db-xref="GI:71037679"
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                                        TVEKNRGRLTVQD"
gene            135879..138116          /locus-tag="Psyc-0114"
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                                        DSNTNQDGMILRDNVWGDIKQDFARRDFSINALY
                                        YQPLKGVVHDFCGALEDIDNKIIR
                                        LLGNAPIRIEEDPVRLLRALRFKAKLGFDFDSEL
                                        AAQFHDGNWSLLEQISPHRLYDET
                                        QKMFTGGYLVPLLPLLFESGAIDSLIIYPPSEPS
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                                        FYAALLWENYLHQLEKAKKRNMPFADAQMHAAGK
                                        VIDRQRIKTAIPKFAEQFIRDIWI
                                        LQPKLAAPRSKQIVQLSEHPRFRAGFDFLLLREQ
                                        CGDAEHPLSESTNDMGEWWQTYQT
                                        LSEQQQDEAIEGFDENIRRGAYKQGQRGRGRNRQ
                                        KQQNSNDNAKPNQIDNDYQDKALS
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                                        YSPQQVAQDNNELAQLQQLSLASS
                                        NNGSNQQHTLKPAPLFVIEHGNVVPPLKKQLSGS
                                        EKILPRAPQKAPMQETAGKKVSAD
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                                        NARTIVHAERNAAQSPALVSMNNE
                                        PIPHKRRRRQPTVIENSGTVAEVSSTKKAVEIDT
                                        NSNDKSAGKYAKKAPKPAADSTDN
                                        AIAKAPKPVKASSAKLAKANRDTGIQSATVQIDA
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gene            138151..138732          /gene="folK"
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CDS             138151..138732          /gene="folK"
                                        /locus-tag="Psyc-0115"
                                        /EC-number="2.7.6.3"
                                        /function="Folate synthesis"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="probable
                                        2-amino-4-hydroxy-6-hydroxymethyld
                                        ihydropteridine pyrophosphokinase
                                        (HPPK)"
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                                        /db-xref="GI:71037681"
                                        /translation="MNMSLTDIHKNSDNSADMNA
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                                        LEQQAKRARLRHWGERSLDVDILLYGDEQVAEPQ
                                        LTIPHAGLHERNFVLIPLRELVPE
                                        LIIAGKSIVDYPQSSDWAGLKLLSNAELSRNQI"
gene            138792..139592          /gene="panB"
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CDS             138792..139592          /gene="panB"
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CDS             139644..140510       /gene="panC"
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                                     LVRDLSYSIEIIGAPIVRAADGLALSSRNQYLSE
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                                     LDTKGVENTAYNLPAAIEKEIQLL
                                     QPICKYADIKIDTSMLNIHQLKERLRDYVGVDNQ
                                     IVINLLSFGFKYGSPIDADFVFDV
                                     RILPNPHWNPTLRAATGLDAEVGEFFADYPEVTE
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gene            complement(142426..1430 /locus-tag="Psyc-0120"
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CDS             complement(142426..1430 /locus-tag="Psyc-0120"
                46)
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                                     SEAMARRGADVTGIDLGTENLKAASLHAEQSNLQ
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                                     TCMEMLEHVPDPAAIVDACFKLLAPGGVCVLSTI
                                     NRNPKSYLFAIVGAEYVLRLLDRG
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CDS             144428..145138       /locus-tag="Psyc-0122"
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                                     SALEEKGVPWGIVTNKPRYLSELLLKKMQLNTRC
                                     AVLVCPDDVSRPKPDPEPMYAALE
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gene            145243..146130       /locus-tag="Psyc-0123"
CDS             145243..146130       /locus-tag="Psyc-0123"
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                                     VDMFAQVMKINFTSTFMLTQALLPLLKDAPQGSI
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gene            146254..146520       /locus-tag="Psyc-0124"
CDS             146254..146520       /locus-tag="Psyc-0124"
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                                     /note="Citation: Brown L, Gentry
                                     D, Elliott T, Cashel M (2002).
                                     DksA affects ppGpp induction of
                                     RpoS at a translational level. J
                                     Bacteriol 184(16);4455-65. PMID:
                                     12142416"
                                     /codon-start=1
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                                     /product="probable RpoS regulator,
                                     TraR/DksA family"
                                     /protein-id="AAZ17998.1"
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gene            complement(146719..1478 /locus-tag="Psyc-0125"
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CDS             complement(146719..1478 /locus-tag="Psyc-0125"
                28)
                                     /note="This protein shows low
                                     homology to the cobalamin
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                                     (PFAM cobW).  No RBS was found."
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                                     DKEIELPYRYHEKQQDIVLAGWRL
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gene            complement(147959..1487 /gene="ompR"
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CDS             complement(147959..1487 /gene="ompR"
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                                     IAGLNRNVAQQIVTYRKEHGAFDS
                                     RESLKNVPRLGAKTFEQAAGFLRIHDGSNPLDAT
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                                     ARDPRPEFKTANFRDDVNSIKDLS
                                     EGMILEGVVTNVTAFGCFIDVGVHQDGLVHISQM
                                     ANDFVADPMNRVKPGDIVSVRVIS
                                     IDEKRGRIGFSMKPEAEKPARPAAKPATAKVTNN
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                                     PSSSNHSDSRSKAPRAEKAEAPSKMGTFGALLQE
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                96)
                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
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                                     probability 0.937 at residue 25"
CDS             complement(151802..1522 /locus-tag="Psyc-0128"
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                                     RVNSNIGQQPMTTEIKAPQKAIQN
                                     LELQTTEIVSEDAVLEAPEDLIEMSEEAPEDLTE
                                     MSEKAPEDLTEISEEAPEDLTEMS EEEL"
gene            complement(152743..1540 /locus-tag="Psyc-0129"
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CDS             complement(152743..1540 /locus-tag="Psyc-0129"
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                                     QVIISTVGPYLKYGEPLIKSCVDNGTDYVDLTGE
                                     AIFIKDMIDKYQEAAKQSGARIVN
                                     SCGFDSIPSDLGVYFTQKQAEAKFDSACDVIHMR
                                     VKAAKGGLSGGTIASMATIFEEVG
                                     QDKSRRKQVANPYLLNDDKDVPNVRQSNVSKPEY
                                     DSEHKRWLAPFVMASINTRIVHRS
                                     NQLLGYEYGRDFKYDEAMWMKDGIKGKLTSYALS
                                     AGLLGFATAMMITPSRELLSKHVL
                                     PKSGSGPSKEEQENGYFDIRLFGKTANKETIATK
                                     VTGDKDPGYGSTSRMLSQAALCLA
                                     QDISKEAVGGGFWTPASAMGDKLLARLKEHAGLS
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gene            154478..154633       /locus-tag="Psyc-0130"
CDS             154478..154633       /locus-tag="Psyc-0130"
                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     0.999) with cleavage site
                                     probability 0.198 at residue 28"
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                                     /transl-table=11
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                                     /translation="MFRWAIIFAVIALLASFLGF
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gene            complement(154919..1552 /gene="phhB"
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CDS             complement(154919..1552 /gene="phhB"
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                                     /locus-tag="Psyc-0131"
                                     /EC-number="4.2.1.96"
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gene            complement(155523..1558 /locus-tag="Psyc-0132"
                16)
CDS             complement(155523..1558 /locus-tag="Psyc-0132"
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gene            156306..157967       /locus-tag="Psyc-0133"
CDS             156306..157967       /locus-tag="Psyc-0133"
                                     /note="probably not a tranpsorter"
                                     /codon-start=1
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                                     /product="ABC transporter related
                                     protein, fused ATPase domains"
                                     /protein-id="AAZ18007.1"
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                                        RLDAIYAEYAEPDADFDKLAEEQGKMEDIIQAWD
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                                        SKLSGGEKRRVALCRLLLSRPDMLLLDEPTNHLD
                                        AESVAWLEQFLQNYSGTIVAITHD
                                        RYFLDNVAQWILELDRGHGYPYEGNYTEWLEQKN
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                                        RKNQKGQQAKSKSRVQRFEELNSQEFQKRNETSE
                                        IYIPPGPRLGNKVIEVNDISKSFG
                                        DRLLYENLSFNVPAGAIVGIIGPNGAGKTTLFNM
                                        ITERDTPDTGSVDLGESVKVAYVG
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                                        YIGRFNFKGSDQQKHVGQLSGGER
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                                        HKLPPALVGVNDSAHNIKENAAIIFLHHPHAKDT
                                        QLSPRLSRLVSAVLQYPQLKVCLV
                                        PVSILWGRAPEKEDSLFKLLTADNWQDPSITKQL
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                                        VYSPAIKHAIEAQAAETGTSPREA
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                                        IPTYIGYERIMEGGTYVGELKGKPKESESLIGLL
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                                        IKVMQHINKAAVVTPVSLLSLVLL
                                        SAPKSALDEDICREQIALYQGLAQQLPYSSDTVV
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                                        EQSLERYFMTLALLAQQGSGNLTENEVVDLCHLL
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                                        LGALTRLDYLQKAAETGILTFDHRINDIAHHAKY
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CDS             161278..161766          /locus-tag="Psyc-0135"
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gene            161842..162216          /locus-tag="Psyc-0136"
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gene            complement(162300..1641 /locus-tag="Psyc-0137"
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CDS             complement(162300..1641 /locus-tag="Psyc-0137"
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CDS             164664..165791          /locus-tag="Psyc-0138"
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                                        RQPPPAGLFVMMAGALALFIPLPL
                                        EQIMSVTGLVMLGSGFALIMGLLYSLFLLATRPA
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                                     SGVSRAEALYGDNTDGQGLVNHMQRLGWPLNGAR
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gene            167146..167811       /locus-tag="Psyc-0140"
CDS             167146..167811       /locus-tag="Psyc-0140"
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                                     LELGWYFANPTDSDKEKKLSQNHA
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gene            167815..168774       /locus-tag="Psyc-0141"
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gene            complement(168785..1689 /locus-tag="Psyc-0142"
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CDS             complement(168785..1689 /locus-tag="Psyc-0142"
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gene            complement(169265..1700 /gene="dpnC"
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CDS             complement(169265..1700 /gene="dpnC"
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                                    GWVGCNIDLRKVAESGKVFLVKDQ
                                    QVIPRDNVTKQFQKTLFLRAQSITSRGWTLDVLQ
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gene            170201..171484      /locus-tag="Psyc-0144"
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                                    EQPQQMVTIEKGQTYYGLLPQWQQEIPLFSATIA
                                    KLYMKTQVDGPLHAGIYQLPENPT
                                    IAEALHVLGQGVKAAMVKVQIIEGKTSKDLYQAL
                                    RDNKGIKKEVLTADSTNASIAQAL
                                    DLVGILPDTVANSNDPIVNHNLEGWFAPDTYYYG
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                                    ENRAPNLPYQSPYEALVMASIIEKETSVEEERPL
                                    VSAVFNNRLNKSMRMQTDPTIIYG
                                    MGSRYEGNIRRKDIDEKTRYNTYQIDGLPPTPIA
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gene            171585..172262      /gene="tmk"
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CDS             171585..172262      /gene="tmk"
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                                        PQQEQARAAADASFESDSKAPEKR
                                        QEKELADDDSNIEEASLIDSDKDAEQNLLNDVPA
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CDS             175485..176942          /gene="mucD"
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                                        probability 0.989 at residue 47"
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                                        DYSASAGIVSAKSRNFSRETSVSF
                                        IQTDVALNPGNSGGPLFNQRGEVIGINSRIFSGT
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CDS             177480..178385      /gene="dapA"
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                                    ADAGADCALLVAPYYNKPPQEGLYQHYKAIAEAV
                                    NIPQMLYNVPGRTVVDIAQETVER
                                    LADLGNIVAIKDATGSVARGEQLIKVVGDRLVVL
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gene            178400..178735      /locus-tag="Psyc-0149"
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                                    QRAVTSRAE"
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CDS             178866..179579      /gene="purC"
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                                    RRLGLEEGQALTPPTYELFYKDDALGDPMVNESI
                                    SISLGWATDAQLAKMKELSHQVNE
                                    VLTALFDAGDLILVDFKLEFGVFHDRIILGDEFS
                                    PDGCRIWDKATKKKLDKDRFRQSL
                                    GDVIEAYEEVASRIGVPLS"
gene            complement(179656..1799 /locus-tag="Psyc-0151"
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CDS             complement(179656..1799 /locus-tag="Psyc-0151"
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gene            180101..180364       /locus-tag="Psyc-0152"
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CDS             180101..180364       /locus-tag="Psyc-0152"
                                     /note="Methylpurine-DNA
                                     glycosylase is a base
                                     excision-repair protein. It is
                                     responsible for the hydrolysis of
                                     the deoxyribose N-glycosidic bond,
                                     excising 3-methyladenine and
                                     3-methylguanine from damaged DNA.;
                                     Probable methylpurine DNA
                                     glycosylase"
                                     /pseudo
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CDS             180603..180914       /locus-tag="Psyc-0153"
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gene            complement(180969..1811 /locus-tag="Psyc-0154"
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CDS             complement(180969..1811 /locus-tag="Psyc-0154"
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gene            complement(181490..1817 /locus-tag="Psyc-0155"
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CDS             complement(181490..1817 /locus-tag="Psyc-0155"
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                                     NY"
gene            complement(181933..1821 /locus-tag="Psyc-0156"
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CDS             complement(181933..1821 /locus-tag="Psyc-0156"
                36)
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gene            182604..182855       /locus-tag="Psyc-0157"
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gene            complement(182842..1841 /gene="dadA"
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                                        /EC-number="1.4.99.1"
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                                        DANLVQMVRLGLYSRDALQQLRADIGVDYEQQTR
                                        GIMHFYTNQAEFDAAIAPTERMQA
                                        LGCERYVIDINNAVSLEPALYPVAHKLKGATYTS
                                        HDESGNAHLFTQRLAEHCIKAGVK
                                        FLYDTEILAINTDDDYAHPHVHSITIRPNGENAQ
                                        TFSADSYVLALGSYSVALMKPLKI
                                        HLPIFPAKGYSATYQINPRAPHLAPFVSLIDDEF
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                                        YWIVAATQGEFQPQELRLHQRGGM
                                        DYDKGCYLGQEVIARIYFKSAPKAFLHYVKGTSV
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gene            185292..185645          /gene="phnA"
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CDS             185292..185645          /gene="phnA"
                                        /locus-tag="Psyc-0160"
                                        /note="Phosphonoacetate hydrolase
                                        PhnA is a novel carbon-phosphorus
                                        bond cleavage enzyme. The phnA
                                        gene is part of a large operon in
                                        Escherichia coli associated with
                                        alkylphosphonate uptake and
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gene            185744..187045       /gene="hemL"
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CDS             185744..187045       /gene="hemL"
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                                     VKFEGCYHGHSDSLLVKAGSGMLD
                                     IGEPTSKGVPADFAKHTITIPYNDSQAIKDCFEK
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                                     FDPLLTESLQMGCVAFTQKYFADGQITKEAFNNA
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gene            189235..190038       /locus-tag="Psyc-0163"
CDS             189235..190038       /locus-tag="Psyc-0163"
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                                     step in the synthesis of
                                     long-chain fatty acids which
                                     involves the carboxylation of
                                     acetyl-CoA to malonyl-CoA"
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CDS             192082..192915       /gene="proC"
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                                     /function="Proline biosynthesis"
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                                     GLSTDVLSSMLGGYRNIVRAMPNTPAMIQMGATG
                                     LYGTDDISAEQKQLATAVMEASGL
                                     VMWVEDEAHMHAVTAVSGSAPAYMFYIIEAMVDG
                                     AVALGLDKEQASALAMQTMLGAAK
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gene            193038..193607       /locus-tag="Psyc-0166"
CDS             193038..193607       /locus-tag="Psyc-0166"
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                                     LVLDFLRMCRYLVIGSIIVSWIVVFTRSEHPIIG
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gene            complement(193860..1946 /gene="thiD"
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CDS             complement(193860..1946 /gene="thiD"
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                                     /EC_number="2.7.4.7"
                                     /function="Thiamine synthesis"
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                                     LFVLDPVLVANSGDSLGDEQTLVTAFRRLLPYAT
                                     LITPNTHELRALSAEQDLHIGAQK
                                     LCAQGTYAVLVKTSHDFDSGDIEQYLYIEGEMVY
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gene            194905..194994       /locus_tag="Psyc_R0003"
tRNA            194905..194994       /locus_tag="Psyc_R0003"
                                     /product="tRNA-Ser"
gene            195179..195255       /locus_tag="Psyc_R0004"
tRNA            195179..195255       /locus_tag="Psyc_R0004"
                                     /product="tRNA-Arg"
gene            195455..196129       /locus_tag="Psyc_0168"
CDS             195455..196129       /locus_tag="Psyc_0168"
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                                     /transl_table=11
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                                     /protein_id="AAZ18041.1"
                                     /db_xref="GI:71037733"
                                     /translation="MSKSLSKRPSKSAAKAQSSN
                                     SVSKMSAHQNSEIEEPTIAKPMAR
                                     VVAILYDGMLILALLFLVGTVLTVIGTLLTMETG
                                     SQSSQAQSLPTWYQNFIMTPSFIL
                                     TLVGFYGLFWRRGGQTLGMQTWRLKTVNNNGYLL
                                     TWGQSFKRIFAASLMPLLFGIIGS
                                     LIGGSRAILLTSAFLGLIFNYAFCLFNRRGLAVQ
                                     DMISNTITLKMPKVEHEGLWRGFR NRKKSR"
gene            complement(196376..1967 /gene="panD"
                56)
                                     /locus_tag="Psyc_0169"
CDS             complement(196376..1967 /gene="panD"
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                                     /locus_tag="Psyc_0169"
                                     /EC_number="4.1.1.11"
                                     /function="Alanine synthesis"
                                     /codon_start=1
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                                     decarboxylase"
                                     /protein_id="AAZ18042.1"
                                     /db_xref="GI:71037734"
                                     /translation="MLLNMLKCKLHRARVTHAEL
                                     HYEGSCGIDGDLLDLAGLRENESI
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                                     ADLGDIVIICAYAHFDEVEASTYQ
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                                        PRLVYCNEDNTVKDTANIIPVQVA"
gene            complement(196856..1974 /gene="pth"
                37)
                                        /locus-tag="Psyc-0170"
CDS             complement(196856..1974 /gene="pth"
                37)
                                        /locus-tag="Psyc-0170"
                                        /EC-number="3.1.1.29"
                                        /function="Peptidyl-tRNA hydrolase
                                        (PTH) is a bacterial enzyme that
                                        cleaves peptidyl-tRNA or
                                        N-acyl-aminoacyl-tRNA to yield
                                        free peptides or N-acyl-amino
                                        acids and tRNA."
                                        /codon-start=1
                                        /transl-table=11
                                        /product="peptidyl-tRNA hydrolase"
                                        /protein-id="AAZ18043.1"
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                                        /translation="MAIKLIVGLGNPGQEYMFTR
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                                        VKFYGIDNDELLIAHDELDIPAGS
                                        IKLKTDGGHGGHNGLRDITPHIGNDFHRLRVGIG
                                        HPGHKSKVSGHVLSKAAPDEQIAI
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gene            complement(197634..1983 /locus-tag="Psyc-0171"
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CDS             complement(197634..1983 /locus-tag="Psyc-0171"
                08)
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                                        VIKDLQRHPAKGFPMHADFQRVVK
                                        GQKINMNVPVHFSGREEAPGTKAGGILSTLVTDI
                                        EIVCIPSQLPEYLEIDVSGMEIGD
                                        LFRLSDIKLPEGVIIFDLDMEDAHDRTIVNMQPP
                                        TVQEVDKVAEIDASDVPATEQGTD GNKDGK"
gene            complement(198705..1996 /gene="prsA"
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                                        /locus-tag="Psyc-0172"
CDS             complement(198705..1996 /gene="prsA"
                52)
                                        /locus-tag="Psyc-0172"
                                        /EC-number="2.7.6.1"
                                        /function="Pentose Phosphate
                                        Pathway -> Histidine biosynthesis,
                                        pyrimidine biosynthesis, and
                                        purine biosynthesis"
                                        /note="Produces
                                        5-phospho-alpha-D-ribose
                                        1-diphosphate, a precursor for
                                        histidine, pyrimidines and
                                        purines."
                                        /codon-start=1
                                        /transl-table=11
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                                        ribose-phosphate
                                        pyrophosphokinase"
                                        /protein-id="AAZ18045.1"
                                        /db-xref="GI:71037737"
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                                        KEHVRGKDVFIMQPTCAPTNDNLMEIMMMADALR
                                        RSSAGRITAVMPYFGYARQDRRPR
                                        SARVPISAKVVADMLNIVSIDRVMTVDLHSDQIQ
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                                     GFFDIPVDNIYGTPVLLNDLQKQN
                                     YDNIMVVSPDVGGVVRARAMAKQLGDTDMAIIDK
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                                     VDDMVDTAGTLCKAAEALKANGARRVVAYITHPV
                                     LSGNALKNISESELDEIVVTDTIP
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gene            complement(199763..1998 /locus-tag="Psyc-R0005"
                38)
tRNA            complement(199763..1998 /locus-tag="Psyc-R0005"
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gene            complement(200082..2001 /locus-tag="Psyc-R0006"
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tRNA            complement(200082..2001 /locus-tag="Psyc-R0006"
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gene            complement(200407..2013 /gene="ispE"
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                                     /product="4-diphosphocytidyl-2-C-m
                                     ethyl-D-erythritol kinase"
                                     /protein-id="AAZ18046.1"
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                                     TLLAAAIDSSKLPEHLPKVLVTLDKHLPMGAGLG
                                     GGSSNAATTLLVLNEIWQLNFNQE
                                     TLIKIGAKIGADVPIFIFGQDAIATGIGEQLTAI
                                     DLPDQQYLVLTPNAHVNTAKLFAH
                                     PKLPRDITLLSIETIKNQYDNYVQTLIAPYHNVF
                                     TPVVTSLAPAVDEGLRYLQGLEKI
                                     ALGTARMTGSGSTVFLPLDASVTDDKLLLSKWIE
                                     EAPCTAYVVRSL"
gene            complement(201438..2020 /locus-tag="Psyc-0174"
                76)
                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     0.981) with cleavage site
                                     probability 0.317 at residue 35"
CDS             complement(201438..2020 /locus-tag="Psyc-0174"
                76)
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                                     /db-xref="GI:71037739"
                                     /translation="MSTLLSSYKPNKLALFTAMT
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                                     SGSAFYAWGQQNDRFAIELIGALG
                                     IGKTNIEYNGQSATLVSEKTGTLTATDPETLLKK
                                     ATGWQAPISQMPYWISGRSAPSDS
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                                     SAVQAQGNKVVMTVNHQK"
gene            complement(202218..2038 /locus-tag="Psyc-0175"
                82)
CDS             complement(202218..2038 /locus-tag="Psyc-0175"
                82)
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                                     AHLALRAHDYDLAGETLNRILSYDPRADLSEILI
                                     GIYPNSDDDKRELLSALQPIASEK
                                     NASLSVLKAGLLYQFNEPEIAIIHINHALEQQPD
                                     YVPFITLKADILRKIETPKAVLDH
                                     LSQAHLRNANSKNLYLYEIRYLLDLKQNEQAWQL
                                     LLDAHQRFADDAEITLLAALVSLD
                                     IEKYASADQLLNTLAKNSAYLDQSHYYLGISAER
                                     QQNFEQAKYYLNAVMQEDLVLEAR
                                     RKVVALDLLNDDVDAAIATLEKMRRDFSVFAPDS
                                     FVLQADILWQQNESAEALLLLTKA
                                     ARKYPNNEMLLFARAQLLDDKEDYIVKRTLLNHL
                                     QALDPTNPAYQLSYAQLLLANERG
                                     SEQGLALATAIIQIRYDDPRYDNERHLQALNVLA
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                                     TLRSGTLLLRAYQGLGDNEKVDALLADLQQRFSF
                                     GQHNINDRIQLY"
gene            204616..205995       /gene="hemA"
                                     /locus-tag="Psyc-0176"
CDS             204616..205995       /gene="hemA"
                                     /locus-tag="Psyc-0176"
                                     /EC-number="1.2.1.70"
                                     /function="Heme synthesis"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="glutamyl-tRNA reductase"
                                     /protein-id="AAZ18049.1"
                                     /db-xref="GI:71037741"
                                     /translation="MRLVVIGVNHKTAPVALRER
                                     LALVGDDVNIALAQLQGFSDGSVI
                                     VSTCNRTEIYALVPESILSPNTLLASSALSVVES
                                     SISLNSSTNISSTIISAHILKIKT
                                     WLADFKQLSLDEIDPYLYVHRDMHALTHWLRVAA
                                     GLDSMILGEPQILGQIKRAVHLAQ
                                     DQKALSNQLGWIVDQVFAAAKRVRNETQVGAQAV
                                     SLSYAAAKLVTQIFDDLPSRTLLV
                                     VAAGEMNRLVAMHIAGLGVGRIIICNRNPERAEA
                                     LAAELRNPKRQIEVRTLQELPQVL
                                     AEADIVSSCSGSMDILIDKTMTLRALKSRRYQPM
                                     LMIDLAVPRDIDSTVSRIDDVYLY
                                     SVDDLQHVIAGNIEQRRQAAVDAELLVSQLVVEM
                                     DRRFQVRQVGKDIQQYRSRTHEQV
                                     DKLLQESIAKLQGDNANPEDIMIELTRRLTQNLT
                                     HAPSKLMRKAAREGDNELLDFVVS
                                     GLQDAHRHH"
gene            206442..207578       /gene="agxT"
                                     /locus-tag="Psyc-0177"
CDS             206442..207578       /gene="agxT"
                                     /locus-tag="Psyc-0177"
                                     /function="Serine biosynthesis and
                                     metabolism"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="possible serine-pyruvate
                                     aminotransferase"
                                     /protein-id="AAZ18050.1"
                                     /db-xref="GI:71037742"
                                     /translation="MTALRQDIDPNGLLEYSVVY
                                     TDRALNHMSKAFQEVMNDLLSNLK
                                     TVYNAEAAVIIPGSGTYGMEAVARQLTIDEDCLI
                                     IRNGWFSYRWTQILEKGKFAKSST
                                     VLTAERTEDTEAPKPFAPVDIETAVAKIKEDKSA
                                     IVYAPHVETSSGIILSEEYIKALS
                                     EAVHSVGGLLVIDCIASGCVWLDMKELGIDVLIS
                                     APQKGWSSTPCAGLVMLSAAAIKK
                                     VESTESNCFSLDLKQWLTIMRAYENGGHAYHATM
                                     PTDSLRQFRDAILEAKEIGFDILR
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                                     DAQWELGNRVRKVLTDKGIESVAAEGFEAPGVVV
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                                     EKALDEVLAK"
gene            207814..208251       /locus-tag="Psyc-0178"
CDS             207814..208251       /locus-tag="Psyc-0178"
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                                     GCTSGHGICGNARLSPRSMAATVTFMFFGIVTVY
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gene            208344..208766       /locus-tag="Psyc-0179"
CDS             208344..208766       /locus-tag="Psyc-0179"
                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     0.953) with cleavage site
                                     probability 0.501 at residue 23"
                                     /codon-start=1
                                     /transl-table=11
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                                     /protein-id="AAZ18052.1"
                                     /db-xref="GI:71037744"
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                                     PGPGIVLLGTGQWQAYVFIPAMIIGMLIYQWLEP
                                     KLNG"
gene            complement(208866..2105 /locus-tag="Psyc-0180"
                30)
CDS             complement(208866..2105 /locus-tag="Psyc-0180"
                30)
                                     /function="catalytic activity"
                                     /note="The family of enzymes
                                     includes luciferase, long chain
                                     fatty acid Co-A ligase, acetyl-CoA
                                     synthetase and various other
                                     closely-related synthetases."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="probable AMP-dependent
                                     synthetase and ligase family
                                     protein"
                                     /protein-id="AAZ18053.1"
                                     /db-xref="GI:71037745"
                                     /translation="MTDFHTGLGKNAANHQPLTP
                                     IDFIIRSAQVYPDRTAIIYDDLEH
                                     NNLTQTWQQTYDRCRQLADGLRKLGVDKNDTVAV
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                                     LNTRLDINALSFCLQHSEAKVLILDSEFAEHAEM
                                     IDETFPNLIVIHATDAAVDIERFG
                                     QMSYEELIASADSLDNWEKPTDEWDAIALNYTSG
                                     TTGKPKGVVYHHRGATLNAVSNIL
                                     DWDMPKHPMYLWTLPLFHCNGWCFPWTIAERAGV
                                     NVCLRKIDADLILQLIAKHKVSHY
                                     CSAPVVHNMIAGGKPEYKEAINHEVKGWVAGAPP
                                     SETMLAAMEAMGFHISHVYGLTEV
                                     YGPVTICAEQQEWATLDVAGRAQKKSRQGVTSHL
                                     MSGFELFKQGTTEPVAADGKEMGE
                                     LALRGNMVMKGYLKSRKATEEAFTDGWFRTGDLG
                                     VKYPDGYIKIMDRLKDIIISGGEN
                                     ISSIEVENVLYKMPEIQSCAVVAAPHDKWGEVPV
                                     AFIEIHAGSTLQRDNVMAHCKQHL
                                     ASFKMPKYIIFAEIPKTSTGKVQKFELRQAAKSL
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gene            210870..213005          /gene="fadH2"
                                        /locus-tag="Psyc-0181"
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                                        /locus-tag="Psyc-0181"
                                        /EC-number="1.3.1.34"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="2,4-dienoyl-CoA
                                        reductase"
                                        /protein-id="AAZ18054.1"
                                        /db-xref="GI:71037746"
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                                        NREGWLLPASGTMNTRADVLNHQR
                                        VTRAVHKYDSKIIMQILHSGRYGYHPFVVSSSPI
                                        KSPISPFKPRKMSIKNIEQTVKDY
                                        ARSAKLAKQAGYDGVEIMGSEGYLLNQFLSRHVN
                                        KRTDEYGGDIQGRMKLAVDVVKAV
                                        REAAGEDFIMLFRLSVIDLVKDGNVMDEVIIVAK
                                        ALEEAGVTIMNTGIGWHEARVPTI
                                        VTSVPRAAFVDFTAEIKKHISIPMMAANRINMPE
                                        TAEEIVASGQADLIQMARPFLADA
                                        HWVNKAKDGQADRINTCIACNQACLDHTFDNKRS
                                        TCLVNPQACYETELVYKKTKKPRK
                                        VAVIGGGVAGMSAAHVAALRGHEVTLFEAKDILG
                                        GQFNYAKVIPGKEEFFETIRYYIN
                                        ELEHLGVEIKLNTKVDKAMLEKAKFHHVIVATGV
                                        VPRSLAGKLEGADLPQVMSYAELL
                                        SGEKSVGATVAVIGAGGIGFDVSEYLTAKHGQPL
                                        DELDPELLKDSSYRPKAQSIEEWR
                                        EEWGVTSATDYQTEGGLIKTGDITPVRQVYLIQR
                                        TKGRLGSGLNKTSGWVHRAHVKSH
                                        GVIQVSGAQYDKITNEGIWITNNQGQSQLLRVDS
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gene            213389..214492          /gene="nemA"
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CDS             213389..214492          /gene="nemA"
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                                        WHTGLVAHESVQPDGKAPISASDVNVGVRTSLRD
                                        SNNQAIRVDATTPRPATLEEIQQV
                                        IADFGLATKNAKEAGFDGVEIHGAHGYLLHQFWV
                                        EHTNQRTDEYGGSRENRARLMLAV
                                        IDACVDAWDADHVGIRISPLGTFNNVEAGYNEDE
                                        NIWLIEQINQRGLMYLHLSEPDWA
                                        GGTPYSTEFRQRVREAFGQMIIAAGGYTAEKAET
                                        NIKDGYIDAVAFGRDYIANPDLAE
                                        RIREGAPLNEQHPQSFYGGGTEGYTDYPFLNQA"
gene            complement(214749..2160 /locus-tag="Psyc-0183"
                65)
CDS             complement(214749..2160 /locus-tag="Psyc-0183"
                65)
                                        /note="Member of TIGR00275 family
                                        of proteins.  RBS found."
                                        /codon-start=1
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                                        /db-xref="GI:71037748"
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gene	216448..218409	/gene="acs" /locus-tag="Psyc-0184"
CDS	216448..218409	/gene="acs" /locus-tag="Psyc-0184" /EC-number="6.2.1.1" /codon-start=1 /transl-table=11 /product="acetyl-coenzyme A synthetase" /protein-id="AAZ18057.1" /db-xref="GI:71037749" /translation="MTQKSFPITPEFLAAANVTA EQYVEQYQQSIASPEATDAFWAKQ AELIDWIKKPTKISDVSYDLEDFRIKWFEDGELN ISVNCLDRHVKNNPYKPAIIWEGD HPSLHKIISFKELHEAVCRLGNAMRKLGVKKGDR VTLYMPMIPEAVVAMLACTRIGAV HSVVFGGFSTQSLGNRIIDSQSKLVITADEGIRG NKRTPLKANVDRALDMDGTDSVSN VIVVHRTGNSVPMSGRRDIWYHSLVDGESQYCEP EVMNAEDPLFLLYTSGSTGKPKGV LHTTGGYITYALSTFRDVFDVKDDDVYWCTADVG WVTGHTYATYAPLANGTTTVMFEG VPEYPTWARIGHIIDKHQITVLYTAPTAIRAMMK EGDTFVRESDRSSLRLLGTVGEPI NPEAWDWYYHIVGGGKCPVVDTWWQTETGGIMLA PIPGTVAMKPGAVMNPLYGIIPEV IDTDGVALEGAAEGNLVINGSWPGQMRTIYKDHA RFLETYFTEYPGYYFTGDGVQRDE DGHYWITGRVDDVLNVSGHRLGTAEIESAIVAHP ATAEAAVVGMPHDIRGIGICAFVI LKSSETATESLKAELNRHVRTEIGPIANLDAIYM VNVLPKTRSGKIMRRILRSLAAGQ YVGLGDLSTLADSSVINELVEVVKTERAK"
gene	219109..219789	/gene="pgsA" /locus-tag="Psyc-0185"
CDS	219109..219789	/gene="pgsA" /locus-tag="Psyc-0185" /EC-number="2.7.8.5" /codon-start=1 /transl-table=11 /product="CDP-diacylglycerol--glyc erol-3-phosphate 3-phosphatidyltransferase" /protein-id="AAZ18058.1" /db-xref="GI:71037750" /translation="MTESTHLPPQETSSTQSNKS IFNLPNNLTIARILMIPLFVAIAY WPPAMGIGMPAISDNVIAKVGMSEFSDSLLRHLL LTGVFILAAITDWLDGYFARKLNV VSAFGRFLDPVADKLMVAAALIILVQWHPNIIMA IAAIVIISREIAVSALREWMAELG KSTSVAVSYVGKLKTTFQMIAITVLLLNWESLET IGYVLMVAAVILTLWSMMIYLKAA WPYLKQSG"
gene	complement(220074..220568)	/locus-tag="Psyc-0186"

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CDS             complement(220074..2205 /locus_tag="Psyc_0186"
                68)
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gene            220986..225014          /gene="purL"
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                                        PELVNDHEMGAVLNLRKIPSLEAG
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                                     RBS found."
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gene            complement(231882..2327 /gene="nadD"
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                                     FRLIGVVPFSDSLSVPRTWDIAAELDATWLNVGE
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CDS             237623..238954       /gene="lysA"
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CDS             239291..240178       /gene="dapF"
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CDS	240236..241273	/gene="xerC" /locus-tag="Psyc-0201" /function="Possible site-specific recombinase that acts on cer sequence of ColE1, effects chromosome segregation at cell division." /codon-start=1 /transl-table=11 /product="tyrosine recombinase XerC subunit" /protein-id="AAZ18074.1" /db-xref="GI:71037766" /translation="MVMSYTNPHVTDAQSDSPSW LSAELALTIEADAALRELLAPVHR WLNVLSVRNHSPHTLTAYFAGLNQLALFLRGKCL TWTRCDKRQLAQHISQRLDEDKLA LASVQQELSAIRHFYGWLIEEDLARINPTTGYQL KRSPRPLPSIADVDLLTQLLDQEI PDTPEQARLWLRDKAMFELLYSSGLRVGELVALD IADVDLADLRVRVTGKGNKTRLVP LGIKAADAIRRYLPHRNLWVEQMDTALFISEKLG TRLSTRAVQQRLKVAATRAGIAQN MYPHLLRHCFASHMLSGSGDLRAVQEMLGHSDIS TTQIYTHVDFAKLTQVYDRAHPRA THASKDSDSTI"
gene	complement(241487..2423 83)	/locus-tag="Psyc-0202"
CDS	complement(241487..2423 83)	/locus-tag="Psyc-0202" /EC-number="3.5.5.1" /function="hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds" /note="Hydrolase conserved domain" /codon-start=1 /transl-table=11 /product="possible carbon-nitrogen hydrolase" /protein-id="AAZ18075.1" /db-xref="GI:71037767" /translation="MSNPINNTQLTVAAIQMNSQ QNIEDNLADIKAAIIEAAAQGAQL AVLPENCCSMGRQFATAEHFDALSAMIAEYARTY GMYVLAGSLPCPYRPDGVIVPDGR LRQASLLFAPDGTRIARYDKIHLFTATVADKQGS YNEAATFEPGAQTVVAALDVEGAV YQLGMMVCFDLRFPALSQRLRQAGAELLSAPSAF TYLTGQAHWSLLLQARALDSQCMV IGAAQGGEHAYKDGHTRQTWGHTTMSAYDGTVIS SYDASELNQSLNEDNKNYAIVLAT LDRQAQNQGRQKMPIFDCHRLA"
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CDS	242863..244572	/gene="rpoN" /locus-tag="Psyc-0203" /function="required for the transcription of promoters that have a characteristic -24 and -12 consensus recognition element but which are devoid of the typical -10,-35 sequences recognized by

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                                     the major sigma factors."
                                     /note="contain all necessary
                                     domains of rpoN except conserved
                                     octapeptide with unkown function;
                                     Citation: Merrick M.J.     In a
                                     class of its own--the RNA
                                     polymerase sigma factor sigma 54
                                     (sigma N). Mol. Microbiol. 10:
                                     903- 909 (1993) [PubMed: 7934866
                                     ]"
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CDS                  244975..245355  /gene="yfiA"
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                                     /note="encoded adjacently
                                     (downstream) from to RpoN (Sigma
                                     54); Citation: Heurlier K et al. J
                                     Bacteriol. 2003
                                     Apr;185(7):2227-35.   PMID:
                                     12644493 [PubMed - indexed for
                                     MEDLINE]    2:  Oosthuiz et al.
                                     Appl. Environ Microbiol. 2002
                                     Jun;68(6):2770-80.   PMID:
                                     12039732 [PubMed - indexed for
                                     MEDLINE]"
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CDS             complement(246097..2464 /locus-tag="Psyc-0206"
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                                     LYWFVHSLGLLLVGILIRLNYATQTAAWLLQIGV
                                     IIFAGSLYAMTLGAPRWFGAITPI
                                     GGVLMIAGWLWLALSSARLTNS"
gene            complement(246530..2475 /gene="rpoH"
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                                     /locus-tag="Psyc-0207"
CDS             complement(246530..2475 /gene="rpoH"
                55)
                                     /locus-tag="Psyc-0207"
                                     /function="DNA binding
                                     (GO:0003677) transcription factor
                                     activity (GO:0003700) DNA-directed
                                     RNA polymerase activity
                                     (GO:0003899) sigma factor activity
                                     (GO:0016987)"
                                     /note="contains the sigma 70
                                     domains 2.2 necessary to bind to
                                     core polymerase and 4.2 necessary
                                     to bind promotor; Citation:
                                     PubMed=6088062; Landick R., etal.;
                                     Nucleotide sequence of the heat
                                     shock regulatory gene of E. coli
                                     suggests its protein product may
                                     be a transcription factor.; Cell
                                     38:175-182(1984)."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="putative Sigma 32
                                     (RpoH)"
                                     /protein-id="AAZ18080.1"
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                                     LVMSHLRFVIHIARSYSGYGLPQADLIQEGNLGL
                                     MKAVKRFDPNKGVRLVSFAVHWIK
                                     AEIHEFVIRNWRIVKVATTKAHRKLFFNLRSLKK
                                     TNNQLTIEEADAIANDLNVTRKQV
                                     LEMESRLTSYDASFEAQSSDDDDGRYAPQLFLED
                                     GIDPAEIVEESDWEENNSSALIAA
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CDS             complement(247635..2481 /locus-tag="Psyc-0208"
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gene            248494..250179       /locus-tag="Psyc-0209"
CDS             248494..250179       /locus-tag="Psyc-0209"
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                                     TRALKLAVSTILLACTSAAYSKSQAAPLSDDSWQ
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                                     NKLLGEWSLRNINGRVKMEHDPWIQETVKELTWR
                                     LNAQARQQAPLGLVIIDNPSINAF
                                     AAPGGVIGLNTGTILAANSMDELASVVAHEVAHI
                                     SQRHYESGADERKKALLMQIGGML
                                     AAIAASTVDGDAAAAVMMGSQTAAMNSSMAFSRN
                                     NERDADRVGMQIMNQAGYDPRAMP
                                     RFFTTMNQKSQMNQTANQFLPSFIRSHPLSNERL
                                     SESQSRAQRYNALPLNQQQRHQAL
                                     FDLLYWRVQSTGKHASEMALMTAAKNSVGAKLAL
                                     MHWYGAQQRFKEADDLFVELSALS
                                     IAKRQVLEPLLSITQSQILTEQNKWQQAAEVLES
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                                     PTKAQVLLKPLTEQQPSDRYAWQSLQLANEKLAK
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                                     WSGHYERALTSLTQAKQLTEKLQNTAQANSARPL
                                     LANINAEIKAVKTAKDFKP"
gene            complement(250391..2508 /locus-tag="Psyc-0210"
                40)
CDS             complement(250391..2508 /locus-tag="Psyc-0210"
                40)
                                     /note="Possible GatB/Yqey domain
                                     (tRNA metabolism). RBS found."
                                     /codon-start=1
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                                     /protein-id="AAZ18083.1"
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                                     KEQFEIDIINEYMPKQMDDAELAA
                                     LVSAEIAEQGATSMRDMGSVMGILKSKTAGRADP
                                     ALISKLVKDALQG"
gene            complement(251039..2512 /gene="rpsU"
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                                     /locus-tag="Psyc-0211"
CDS             complement(251039..2512 /gene="rpsU"
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                                     /codon-start=1
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                                     /product="SSU ribosomal protein
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gene            251670..252038       /locus-tag="Psyc-0212"
CDS             251670..252038       /locus-tag="Psyc-0212"
                                     /note="Signal peptide predicted;
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                                     HMM (Signal peptide probabilty
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                                     TDATMSTEEGAAVVEGTAADATAS
                                     VDSTDTAMAPADSAAMPATN"
gene            252105..252626       /locus-tag="Psyc-0213"
CDS             252105..252626       /locus-tag="Psyc-0213"
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                                     c-terminus; Signal predicted by
                                     SignalP 2.0 HMM (Signal peptide
                                     probabilty 1.000) with cleavage
                                     site probability 0.417 at residue
                                     34"
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                                     EKQCKVCHEKGLLAAPVFGNKEAWAPRIAKGIDT
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                                     VHAAVDYMVAAVS"
gene            252902..253951       /gene="ygjD"
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CDS             252902..253951       /gene="ygjD"
                                     /locus-tag="Psyc-0214"
                                     /EC-number="3.4.24.57"
                                     /function="proteolysis and
                                     peptidolysis"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="O-sialoglycoprotein
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                                     /protein-id="AAZ18087.1"
                                     /db-xref="GI:71037779"
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                                     YGGVVPELASRDHIRKLVPLFNELLAQCNISKDE
                                     IDAIAYTKGPGLIGALMTGALFGR
                                     SLAYGLDIPAIGIHHMEGHLLAPLMGLNPPAFPF
                                     VSLLVSGGHTLLIAAHGIGQYEIL
                                     GESIDDAAGECFDKAAKMLGLPYPGGPNIAKLAE
                                     NGNPNAYSLPRPMLHRGLDFSFSG
                                     MKTAVHNLIKDTDGSGNGSDSDPQVRADIAASFQ
                                     HAVVDTLVKKCVKALKQVDMSRLV
                                     IAGGVSANSHLRETLERELAKINATVHYAPPALC
                                     TDNGAMIAYAGYERLQAGQSDDLA
                                     VSCVPRWPMTELPAV"
gene            254011..254382       /locus-tag="Psyc-0215"
CDS             254011..254382       /locus-tag="Psyc-0215"
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                                     protein CrcB"
                                     /protein-id="AAZ18088.1"
                                     /db-xref="GI:71037780"
                                     /translation="MQWLAIGLGAAFGACLRGWL
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                                     LHVGMTLLATALGFYCFKLVL"
gene            complement(254413..2553 /gene="metR"
                03)
                                     /locus-tag="Psyc-0216"
                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     0.817) with cleavage site
                                     probability 0.371 at residue 24"
CDS             complement(254413..2553 /gene="metR"
                03)
                                     /locus-tag="Psyc-0216"
                                     /function="The majority of these
                                     proteins appear to be
                                     transcription activators and most
                                     are known to negatively regulate
                                     their own expression."
                                     /note="All possess a potential HTH
                                     DNA-binding motif towards their
                                     N-termini."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="putative transcriptional
                                     regulator,  LysR family"
                                     /protein-id="AAZ18089.1"
                                     /db-xref="GI:71037781"
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                                     DISLVNRRTRPLTFTPAGKTVLALADSIMPQVAR
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                                     CFDWLMPILNYYRREWSDVELDFATGFEPEPHHL
                                     LMEGDIDLLITTSNLPIEGISYQP
                                     LFEYESRLVLSPTHDLAEQHFIHPNDLIEETLIA
                                     YPVEAKRLDIIANFMTPEQVSFKA
                                     IRTTELTAMLIQLVASERGVAALPDWVVAEYEKK
                                     GWVVSRPLGDGVYCQLYAATRSSS
                                     QDTAYMQGFASLLEGIVKPV"
gene            255969..256607       /locus-tag="Psyc-0217"
CDS             255969..256607       /locus-tag="Psyc-0217"
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                                     /db-xref="GI:71037782"
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                                     GNVVAPSQIGSVEFAAEKFGTKLV
                                     VVLGHSHCGAVTACVEALINPEKNYSPNLQSIVD
                                     RIRPSVYNLHELATANGQDVDADE
                                     LVDRSIRANVHMSVSQLKHGSRALEDLTSSGQLL
                                     IVGAEYDLETGKVRFLDA"
gene            256690..257259       /gene="gloA"
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CDS             256690..257259       /gene="gloA"
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                                     /EC-number="4.4.1.5"
                                     /function="Pyruvate metabolism,
                                     Lactate biosynthesis"
                                     /codon-start=1
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                                     LAKLTESERENLPSGNDLEIFAFR
                                     QRGILELTHNYGTETKADFSYHDGNQEPQGFGHI
                                     CFNVPDLNAAVAWFDENHVEFKKR
                                     PDEGSMKNIVFIKDVDGYWIEIVQADLMA"
gene                 complement(257347..2583 /gene="hemF"
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                                     SATARHPDIAGRKAQAMGVSLVVHPKNPNVPTSH
                                     ANVRLFIAEAEGKDPIWWFGGGFD
                                     LTPFYPVLADCIHWHQVCHDLCAPFGDTVYPDFK
                                     QWCDEYFHLRHRDEQRGIGGLFYD
                                     DVNTESRGWDFETCFKFMQAVGNGYLEGILPIFE
                                     QRKNAPYTEAQREFQLYRRGRYVE
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                                     RFEPIEGTPEFELTDFYLKPRDWL IL"
gene                 complement(258376..2590 /gene="ribA"
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CDS                  complement(258376..2590 /gene="ribA"
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                                     /EC-number="3.5.4.25"
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                                     /protein-id="AAZ18093.1"
                                     /db-xref="GI:71037785"
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                                     DTTDSLPSPDTILNQEDNALSERPIPLIRIHSEC
                                     LTGDAFSSLKCDCGPQLNTAMHAI
                                     QETGCGAILYLRQEGRGIGLTNKIRAYALQDQGH
                                     DTLDANLMLGLPADARIYDMCGPM
                                     LAHIGVDAVRLITNNPSKVAYLTEHGIDVIERVP
                                     LVVGVNDMNAEYLATKRDRMGHLL
                                     DTDFNTTLHLNK"
gene                 259652..261694          /gene="dxs"
                                     /locus-tag="Psyc-0221"
CDS                  259652..261694          /gene="dxs"
                                     /locus-tag="Psyc-0221"
                                     /EC-number="2.2.1.7"
                                     /function="Catalyzes the thiamine
                                     pyrophosphoate-dependent acyloin
                                     condensation reaction between
                                     carbon atoms 2 and 3 of pyruvate
                                     and glyceraldehyde 3-phosphate to
                                     yield 1-deoxy-D-
                                     xylulose-5-phosphate; synthesis
                                     isopentenyl diphosphate"
                                     /codon-start=1
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                                     /transl-table=11
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                                     sphate synthase"
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                                     PQDQIVWDVGHQAYAHKVLTGRRDRLGTIRSKAG
                                     LTAFPERAESVYDTFGVGHSSTSI
                                     SAGLGMSLALRYQGRAQTVACIIGDGAMTGGMAF
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                                     DVMFAIDRAGLVGEDGATHAGVFDFAFLRCVPNM
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                                     EKDAPKKLALLAFGTMVATAQQAA
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CDS                  262183..263010  /gene="suhB"
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                                     FCVSIAVQHKGVTQHGVIYDPVRDEMFSASRGKG
                                     ARLNQRRISVSERKTIDGGLFTTG
                                     HPLERKRNGEIISYAKEHYESLQKITEAGGQIRR
                                     LGSAALDLCYVAAGRFDGYFEMSI
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                                     FACNIKLLKPLMQVVVPAWGDAL"
gene                 complement(263057..2644
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CDS                  complement(263057..2644
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                                     /product="Diacylglycerol
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                                     GRLLDRAMPLWECHVIEGIQPETEGSPERFALYF
                                     KIHHSLVDGIAAMRLVKKSLSQSP
                                     NEPVTLPIWSLMAHHRNQIDAIFPKERSALRILK
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                                     YVSTFDAPRSILNRRISASRRIAAQSYDIKRFND
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gene            complement(264531..2653 /gene="thiG"
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CDS             complement(264531..2653 /gene="thiG"
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                                     /function="Biosynthesis of
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CDS             complement(265553..2662 /locus-tag="Psyc-0225"
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                                     SVHAVAITLLAETATGFILGLNLPSDRVLLIKSY
                                     SLNFYRPIKKGQMAAIASLSDEQR
                                     LDILNTPKGEMVIPCVIHDRESDSDRDPIVVEMT
                                     WAWIPKSELEARRQGKANEKSAEV
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gene            266672..268168       /locus-tag="Psyc-0226"
CDS             266672..268168       /locus-tag="Psyc-0226"
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                                     for DNA repair"
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                                     AQNAREKNLSNTAWTVLQMHSPTSSQTVTYKNRA
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                                     ALSEQLSEFQQAQYDNNASQHAPSQQQRFSMVSF
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                                     NSLSQMSYGIIDGAFLKLCQRAANDPQQRYAMLI
                                     DEINRANVSRVFGELLSLIEPDKR
                                     VGTANAMTVNLAYSGRTFGVPANVDIYATMNTQD
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gene            268184..269728       /locus-tag="Psyc-0227"
CDS             268184..269728       /locus-tag="Psyc-0227"
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                                     AALPLSDWLITQFLQRLAHHQPITHYQTQIHNQT
                                     ALQGRLLIKEQLRHNSMQPHKFVC
                                     ERSVLSKGMLANRIIKSALKLLAPLLSQSNLLLY
                                     LQPWQQVSVLHQYEIRQLASIYFQ
                                     AKHELAIQPLQAQQLQAAQQLVDFAYWLLCQSHA
                                     ETGHSIDSQNPFHKKLTPQRLCLL
                                     IDMNQAFEQWASQRIALFFQQLSDDYKPLFQTQR
                                     VWLNDAEGQACLSIRPDLLIYKQI
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gene            269965..270041       /locus-tag="Psyc-R0007"
tRNA            269965..270041       /locus-tag="Psyc-R0007"
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gene            270136..270212       /locus-tag="Psyc-R0008"
tRNA            270136..270212       /locus-tag="Psyc-R0008"
                                     /product="tRNA-Arg"
gene            270252..270327       /locus-tag="Psyc-R0009"
tRNA            270252..270327       /locus-tag="Psyc-R0009"
                                     /product="tRNA-His"
gene            270938..272026       /locus-tag="Psyc-0228"
CDS             270938..272026       /locus-tag="Psyc-0228"
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                                     /db-xref="GI:71037793"
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                                     QENSAQAGVVTLLDKAALLALFVLPNAEGSLTET
                                     NSANINTANHTLINQSSTTSASDS
                                     SVATQRVALYRAQHQRTQQLYLASAAIRPTYLVQ
                                     TLKTQFAEYQQYLLAQQLDKRGLM
                                     DTDAIERLWQQLHVVDDIIEDIVRHMPAQQPAGW
                                     QLTTQDGHNPLCFATVGKLKHHKP
                                     IFDQGSLNSYVLGHFGVSSFTYDRGYYIGHVVGY
                                     LFSCYFCAHLSISYGVTALGQDVV
                                     SDYDYASLETPHMVRLLQGLDGYCKKRIYQLAVI
                                     CARLSVFASDKRIERMLIAEVNDF
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gene            272937..273497       /locus-tag="Psyc-0229"
                                     /pseudo
CDS             272937..273497       /locus-tag="Psyc-0229"
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                                     protein; Signal predicted by
                                     SignalP 2.0 HMM (Signal peptide
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                                     /pseudo
                                     /codon-start=1
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CDS             273557..275746      /locus-tag="Psyc-0230"
                                    /note="thiol-disulfideinterchange
                                    protein; Signal predicted by
                                    SignalP 2.0 HMM (Signal peptide
                                    probabilty 0.999) with cleavage
                                    site probability 0.648 at residue
                                    61"
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                                    /codon-start=1
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gene            276220..277656      /gene="pldA"
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CDS             276220..277656      /gene="pldA"
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                                    /EC-number="3.1.1.32"
                                    /note="Signal predicted by SignalP
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                                    1.000) with cleavage site
                                    probability 0.980 at residue 48"
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                                    /transl-table=11
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                                    SERGTWNIRPHNPNYVLPLFYTADPNLSPNTPSQ
                                    DQEQANFTSNNVRQAELKFQLSLK
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                                    FRATDYQPEVFLTQPVTANLPFGG
                                    RLRMLGVGAVHHSNGRSEPLSRSWNRIYLMGGAE
                                    WGKFSIVPRVWARVDGGSSNDDNP
                                    DIEDFMSYGDIKFLYDLPNQQSLSGTLRYHPGTN
                                    KGSAQIDYVYPLTKSVNGYVQLFQ
                                    GYGESLIDYNYENTAVGVGIVLNDWKGF"
gene            277687..278529      /gene="comF"
                                    /locus-tag="Psyc-0232"
CDS             277687..278529      /gene="comF"
                                    /locus-tag="Psyc-0232"
                                    /function="natural transformation
                                    with exogenous DNA"
                                    /codon-start=1
                                    /transl-table=11
                                    /product="possible competence
                                    protein F"
                                    /protein-id="AAZ18103.1"
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                                    SLFSQNSLLAENTSHSLSNNHSFFTNIRKQFHSR
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                                    IAADTTLPIQAATYYDYPMRQAIRAFKHHEDMTK
                                    LPLLLHALRQLPRPHGCHQDNSVI
                                    VAMPTTDERLIKRGFDPVSILAAHLSKHWDIPLW
                                    QGIKRIDNTLSQQGLTRAERLSNL
                                    NNAFILIEPSPVKRLILFDDVATTGASLQALART
                                    LSIYPATTHNANNKCHLYAYVLAH GSQS"
gene            278992..279450      /gene="fimT"
                                    /locus-tag="Psyc-0233"
CDS             278992..279450      /gene="fimT"
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                                    /note="Signal predicted by SignalP
                                    2.0 HMM (Signal peptide probabilty
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                                     0.751) with cleavage site
                                     probability 0.319 at residue 26"
                                     /codon-start=1
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                                     /product="possible type IV pilin
                                     protein"
                                     /protein-id="AAZ18104.1"
                                     /db-xref="GI:71037796"
                                     /translation="MSSSGFTLIELMVTIAVLAI
                                     IVSIAAPSISTQLANQRVKSTTAT
                                     LENALKEAKAESIIRRQKVTVSYNNMSNPKVIIL
                                     TGSDTNASTIASYNYNASSTLTSS
                                     PATATVTFEPSKRVTATITYTICDTNTAANPRQI
                                     VVSRVANITNQMGVTC"
gene            279450..280100       /gene="pilV"
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CDS             279450..280100       /gene="pilV"
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                                     /transl-table=11
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                                     /protein-id="AAZ18105.1"
                                     /db-xref="GI:71037797"
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                                     VDTKTISRSGTDNCLSTGTTNDANGKKIPNKLCN
                                     INQLAARDALMVKKMAADEDIKMA
                                     IVTCPGTTTQSIQTQMCVITAWNDTKAMMNNDDT
                                     KACANSDGVYKTGSHCLISEAY"
gene            280100..281011       /locus-tag="Psyc-0235"
CDS             280100..281011       /locus-tag="Psyc-0235"
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                                     /transl-table=11
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                                     /protein-id="AAZ18106.1"
                                     /db-xref="GI:71037798"
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                                     TTLLTNSMGSTGWTGISNITNVASDQLTIQYKNI
                                     TPNILYDCEGTVIPVNDTNWVIER
                                     YFVRAISTTVPDLALACDAGRATDAGAVTNFGDN
                                     GEVIIQAVDQFQVLLGAQADVNNL
                                     TYLPAKTYLELTDKPAITTVKVGVIVRSTTPLIA
                                     EADKETFTVLGTTQTLKTDSSRKK
                                     FYRRAYESTVLLRNARVMSVIAVATAP"
gene            281023..281841       /locus-tag="Psyc-0236"
CDS             281023..281841       /locus-tag="Psyc-0236"
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                                     /transl-table=11
                                     /product="possible pilus assembly
                                     protein PilX"
                                     /protein-id="AAZ18107.1"
                                     /db-xref="GI:71037799"
                                     /translation="MSHIQQSQYPKSQQGAVLIV
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                                     LSTSDQINALLLQSADNANQNIEQSINGNSNTDI
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                                     EYVFCFRPRGRFFDINKASILTPSGTVFGANSGY
                                     CNPTQSADYVSSRNASMTQVSVSL
                                     TPPNFSNEAFSSYTIGQDSGEIASQAFMFDIHST
                                     AVLPAYADATVGSDNCFEQTSRLH
                                     TVTDSKKTIGGCMAEAGVPSTVVYEQVNVENQSL
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gene            281921..285676       /locus-tag="Psyc-0237"
CDS             281921..285676       /locus-tag="Psyc-0237"
                                     /note="Signal predicted by SignalP
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                                     0.999) with cleavage site
                                     probability 0.426 at residue 35"
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                                     /protein-id="AAZ18108.1"
                                     /db-xref="GI:71037800"
                                     /translation="MKYLYNKNSARQPWPTKSLT
                                     IAVLLSLTAMVSQTAGSVERLPIG
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                                     GNVEVYFTPKGCETTQGGGTSNPKEFDRLSRLQM
                                     ALIELLADQVRNKTGNEFRTGIGS
                                     IPNEYAIGVGIFGYNGTKAKIVAPLGQLTPDRRI
                                     EIIKVIAGLSVASGDGKPTAHGLA
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                                     YISPLELKQCSGNGIYLLTDGVPS
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                                     GDGTWGCMAEYTQKLRDPTNPRLL
                                     PIKTATAGFGDNFKGLTTTRKITVGGKQVEAVDC
                                     SQGAATEVTDDARNLCKLGQRYGD
                                     NELSTNTSVFGNGGFYYIAGEQGKSNVTTEELKS
                                     SKIIENSIVDFASTLTQVITTSPS
                                     GTISIPDDPYRASNQLPYAYLPMLSPDIASSASI
                                     WKGNLKKYHLDAGTLYGKSDQLLY
                                     KNAAGQLNETTQDLWQLTDFTPVGTTTVDNSSIE
                                     AGGVYAQLRTPMSGLASVRTLYVE
                                     DVTSATDSKPILRKLSVNASGKPVGFSSLVDSLY
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                                     GLATSRTAVESLTLTQPVQITRVLGGVVHSKPTA
                                     ISYSSTLNDNGSIIDPRDDYALFG
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                                     NGSKKNQIGQPYFGVDAPWLVTTD
                                     YTYDLAAKKATLDTANSKGMFAYGGLRMGGSAFY
                                     GMNITDKTAPKILFTITPATIGFS
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                                     AYEDDEYVATAAAPATATAPATAA
                                     APAKGNAIYIINAKTGALIWSTSYNLTNNSNMIH
                                     SIVGGITVLDRDNDGLMDHLYAAD
                                     LGGQVFRADFENARPAKFGFSEVTGFSSKRVIRI
                                     LNTTPSAAADSKYTYRFYERPVVS
                                     FYRNEGGPNNGKIFALVNVISGNRSVPLSTLRDG
                                     NTYANRVYGIIDSDVTKASLYDAT
                                     PTLNVTNLTESNLVNLATTLGATPTEAIKKTAKA
                                     EMIAGTKQGWYYPLTRFDGFNNVR
                                     YNKGIGDSVVINDLLYTTVYNPDKQYYEVNNCTA
                                     RISGGSERQLYCLPYGICMDANSV
                                     SGTGGYIPAGEGIKELTLGAYNKNNTNLRVLIGT
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                                     NIKGIVYADQGKPTQGDTNSIGDGSAPEYLFNER
                                     YTLQPRAWYERAQ"
gene            285723..286310       /locus-tag="Psyc-0238"
CDS             285723..286310       /locus-tag="Psyc-0238"
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                                     /product="possible pilus assembly
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                                     /protein-id="AAZ18109.1"
                                     /db-xref="GI:71037801"
                                     /translation="MSKIKSASDANSVRGFTLLE
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                                     YVPNGSTATNYRYKITLVDGTNTAKSLAPSASST
                                     TTTVDSITGRSWKMLATPNTTGIT
                                     ANANHIVLASRGLHCQNKTAVTLAATDCGSGQEE
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gene            286310..286747       /gene="pilE"
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CDS             286310..286747          /gene="pilE"
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CDS             287088..287507          /locus-tag="Psyc-0240"
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gene            287641..288054          /locus-tag="Psyc-0241"
CDS             287641..288054          /locus-tag="Psyc-0241"
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                                        C"
gene            288187..289947          /locus-tag="Psyc-0242"
CDS             288187..289947          /locus-tag="Psyc-0242"
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                                        /transl-table=11
                                        /product="conserved hypothetical
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                                        /protein-id="AAZ18113.1"
                                        /db-xref="GI:71037805"
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                                        LTCVAVSICVANAPNKAKLFQILMWLMVSAGVLT
                                        ALTQIAQYLRLDLPMYLLYPNSAG
                                        ARISANISQPNQAAFILALSTGGLLYLSSLCKGV
                                        FKSSLIVLPSFLLAIGLGLSASRT
                                        GLILMVIAILGYFLLFKLPVKIKVITASACTTLL
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                                     YKVLVRSADIYLLADDKNRALELYKNACIFNYAQ
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gene            complement(290109..2906 /locus_tag="Psyc-0243"
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CDS             complement(290109..2906 /locus_tag="Psyc-0243"
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                                     ERGIWQRRFWEHRIRDDADYRQHMDYIHNNPVKH
                                     GYVTNPQDWQYSTLHTLIKKGVYP
                                     AGWGTDENDKSINIRYDS"
gene            complement(290794..2909 /locus_tag="Psyc-0244"
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CDS             complement(290794..2909 /locus_tag="Psyc-0244"
                19)
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CDS             complement(290940..2916 /locus_tag="Psyc-0245"
                41)
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                                     /translation="MTMTKRTYTPIASTAAKCHL
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                                     TSVAPIVHKFIQSGYETATNIIIVKSVMSGSCVV
                                     RTNLIEMIDDMPNVENIFILAPVA
                                     HRYSEEKLKSEFPATISNKFKFICFAIDEQRSEG
                                     GEVIPGIGGQVYELLGLTDQPVLT
                                     AYMPQVVEKLAFADI"
gene            complement(291832..2921 /locus_tag="Psyc-0246"
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CDS             complement(291832..2921 /locus_tag="Psyc-0246"
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                                     /transl_table=11
                                     /product="ferredoxin, 4Fe-Fs
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gene            complement(292249..2954 /gene="mutS"
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                                     /locus_tag="Psyc-0247"
CDS             complement(292249..2954 /gene="mutS"
                25)
                                     /locus_tag="Psyc-0247"
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                                     is named after the Salmonella
                                     typhimurium MutS protein that is
                                     involved in replication repair and
                                     plays a role in preventing
                                     recombination between
                                     non-identical sequences."
                                     /note="Mismatch repair contributes
                                     to the overall fidelity of DNA
                                     replication MEDLINE:87297443. It
                                     involves the correction of
                                     mismatched base pairs that have
                                     been missed by the proofreading
                                     element of the DNA polymerase
                                     complex.; Citation: Tachiki H,
                                     Kato R, Masui R, Hasegawa K,
                                     Itakura H, Fukuyama K, Kuramitsu
                                     S. 1998. Domain organization and
                                     functional analysis of Thermus
                                     thermophilus MutS protein
                                     [erratum: 1998, 26(20):following
                                     4789]. Nucleic Acids Res
                                     26:4153-4159."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="DNA mismatch repair
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                                     /protein-id="AAZ18117.1"
                                     /db-xref="GI:71037809"
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                                     FHAADSYMARLIAAGQTVVVCEQIDESATGNARN
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                                     TQTLSANHDDIEGLKTQMLTVLARFAPSECIIGE
                                     ALNDSIGGIGEDWLLWLRQSLDCP
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                                     VPQINQLIVEYSDDYLIIDANSQQNLELFTPVSS
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                                     LESQLPSLKVGFNKVSGFYFELPKMQAKNAPAHF
                                     IRRQTLKSSERFITDELKDVETEY
                                     LSAQTLALTREKQLYHELLTELSSHLAELQQLSA
                                     AIAQIDVLSNWAQLAMTYNWQCPV
                                     MSNNDENKDSSNTDNQASIDISQGRHVVVEAALN
                                     PVNAGNAGNTVNSSNNSSNNSGTT
                                     RHNSHFVANDCALGSDANPERLLLITGPNMGGKS
                                     TYMRQTALIVLLAHCGSFVPAASA
                                     HIGDIDRIFTRIGSADDLAGGKSTFMVEMIETAN
                                     ILNQATNQSLVLMDEVGRGTATTD
                                     GLAIAHACVNRLLEIGCLTLFATHYFELTKLAQN
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                                     QLLLLHQIKEGAASSSFGLHVAKMAGIPTQVLND
                                     AKRYLVDNLTIDNLGIDNLSIDNL
                                     KSNNESANDDKNDLAKSVKDKRQQTADSDIEKLN
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gene            295988..298777       /gene="secA"
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CDS             295988..298777       /gene="secA"
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                                        KTGEGKTLMGTLAMYLNAISGKGVHLVTVNDYLA
                                        ARDAELNRPLFGFLGMNVGVIYSQ
                                        QPPQEKVAAYQADITYGTNNEYGFDYLRDNMVFS
                                        LREKKQRPLNFCIIDEIDSILIDE
                                        ARTPLIISGQAEDSSRMYALINTIIPVLIRSKDE
                                        EANKNNEEEDFWIDEKNRQIEISE
                                        KGYEKIERFLIEVGELGENESLYSPSRLPLLAHV
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                                        IVDENTGRTMPGRRWSEGLHQAVEAKENVEIQAE
                                        NQTLATTTFQNFFRLYDKLSGMTG
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                                        PVLVGTATIEASEELSYLLDQEGVKHNVLNAKQH
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                                        IDNQLRGRAGRQGDPGMSRFFLSLEDDLMRIFAG
                                        DRVVNMMRAMGLKEDEAIEHKMVS
                                        KSIENAQGKVESRDFDARKNLLKYDDVANDQRKV
                                        IYGQRDDLLAEMDLLQAIKIMHQE
                                        VYNAMINQFIPPGSIDDQWNVDGLEDELENEFKI
                                        AMPINDWLDEDRRLDEEGLRAKLI
                                        QTALDRYDNRREQMGEKEAAQLERHFMLQSLDKH
                                        WKEHLTQMDQLRKGIHLRGYAQKN
                                        PEQEYKRESFELFQMMLGAIKSETVQDLSRVHIP
                                        TKEELAALEVQQRENAAHMQMQFE
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                                        PCGSALKYKQCHGKI"
gene            299100..299612          /locus-tag="Psyc-0249"
CDS             299100..299612          /locus-tag="Psyc-0249"
                                        /note="Signal peptide predicted;
                                        Signal predicted by SignalP 2.0
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                                        0.986) with cleavage site
                                        probability 0.971 at residue 28"
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                                        EQAVPMSAEPAEPSDVAASEVADDTVATVNTGVN
                                        QITYLCSPELAVEATYKDTDNQVV
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                                        VQWRVAHQDRKTGVMRTAGTDTTN
                                        VTTYECKKTQ"
gene            complement(299711..3003 /locus-tag="Psyc-0250"
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CDS             complement(299711..3003 /locus-tag="Psyc-0250"
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                                        ELVEEYITVRTEYHDTESQDLLSGNYDDKDILRH
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gene            complement(300687..3015 /locus-tag="Psyc-0251"
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CDS             complement(300687..3015 /locus-tag="Psyc-0251"
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                                     YQYSYKEQYERDRQAFIADSVPEAERMEIADHNY
                                     DAPNTLELLEQRLTVNKDRIVAGL
                                     VKVGKHVVTEERNVNVDLEEEHANIERTNVNRPT
                                     ERRIGDIDDNQTIEVEVELEAERA
                                     HVNKETYVTEEVNVGKTTERHTETIVETIQREEL
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gene            complement(302075..3032 /locus-tag="Psyc-0252"
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CDS             complement(302075..3032 /locus-tag="Psyc-0252"
                56)
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                                     GIKAGSFKVAVAGGMESMTNAPYIMPGSRGGYRM
                                     GHKEVKDHMFLDGLEDAETGKLMG
                                     MFAQEVADEKGYTREQMDDFAIESLSRALTAIKD
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                                     GAAAVVLMKESQAKEEGLDYQARI
                                     IATASNSRHPSEFTIAPVGAIEKVLASAGWSVAD
                                     VDLWEINEAFAMVTMVAMDELNIE
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gene            complement(303315..3046 /gene="hom"
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CDS             complement(303315..3046 /gene="hom"
                61)
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                                     /EC-number="1.1.1.3"
                                     /function="Threonine biosynthesis,
                                     Lysine biosynthesis"
                                     /note="Monofunctional enzyme
                                     (hom).  Contains no aspartokinase
                                     domain."
                                     /codon-start=1
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                                     /product="homoserine
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                                     IRRQRDDIDPNIIQNSDLMATAASDNVDIVIELI
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                                     KALLAEHGNEIFAFAEQHNVHVAYEAAVAGGIPI
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                                     LRVHAYDSPGVLADITRILSDAGI
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gene            complement(304875..3057 /gene="dsbC"
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CDS             complement(304875..3057 /gene="dsbC"
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                                     /EC-number="5.3.4.1"
                                     /function="Required for disulfide
                                     bond formation in some periplasmic
                                     proteins."
                                     /note="Citation: Proc Natl Acad
                                     Sci U S A. 1992 Jul
                                     1;89(13):6210-4.
                                     http://www.cf.ac.uk/biosi/staff/eh
                                     rmann/tools/ecce/Peripla
                                     smicBySize.html"
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                                     TAEGLPAFFTDKAGKHIIQGQIIAVGAKAPVDIS
                                     GTLVARTAQDALKAVDKKDMVIYP
                                     AKGATKAVVYAFTDADCPYCAKLHEEMEDINARG
                                     IEVRYLAWPRSEGSIPKMEAIWCS
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                                     ISAIYPPLITFLLMCGGLFLVYEG
                                     AEKVIHRFWPHVLPHDEEQEAHRKANADETVDLV
                                     AFEKEKIKGAIRTDFILSAEIIVI
                                     VLGATASATLLERSLVLSILAISITVGIYGLVAG
                                     IVKIDDVGLHMMEKEGAFIQKVGK
                                     VLLSAAPKLMKFLSIAGTLAMFLVGGGILVHGIN
                                     FLYHGVEDIAHLTGIFASFTTALL
                                     NGVIGFIIGAAIVAILTVVNKMRNKDESAAH"
gene            complement(307312..3115 /locus-tag="Psyc-0256"
                29)
CDS             complement(307312..3115 /locus-tag="Psyc-0256"
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                                     /EC-number="3.1.4.-"
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                                     KEERGNKGAALSTYVSLAGRYLVLMPNNPRGGGI
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                                     MSVIIRTAGIGKTQEDLQHDLNHLLNIWQAIQEQ
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                                     RKYTDYEPMFSRFNIEKQIETAYQ
                                     REVRLPSGGSIVIDQTEALVSIDINSAKSTKGSD
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                                     RVQFGDISKFGLMEMSRQRLRPSL
                                     EESTGYICPRCHGNGMIRDLRSLSLSIMRQIEQI
                                     ALKERQGEVQAEVPTDIAAFLLNE
                                     KRDSLVYLEQDSGTRITILPHAHLESPNFKLHFN
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                                     FAQAPQAQTTSSVSSRDAAEAIEALVNTGAQSLG
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                                     TSVEPRAISKRASNDPRGQHPDYK
                                     ESAVLTVVDPANNEPVQTGIDIDANKVEADALAN
                                     QAQTDAVSDQSKQLLDAEQTPAEV
                                     DTVQADESIVAPFSKEDSQAAKSKTTIASYKNMI
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gene            312743..313759       /gene="rlu"
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CDS             312743..313759       /gene="rlu"
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                                     /EC-number="5.4.99.-"
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                                     /transl-table=11
                                     /product="ribosomal large subunit
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                                     /protein-id="AAZ18127.1"
                                     /db-xref="GI:71037819"
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                                     QSADDEISNFGKVNYLEVTRHQHD
                                     QRLDNFLLNRLKGLPKPHIYKMIRSDEIRVNNKR
                                     CKAHDRVQREDVVRIAPVVLATRE
                                     KPIISTEFAKSLLARVVYEDEGLIVLNKPSGIAV
                                     HGGSGLDFGVIEAMREVTGKKYLE
                                     LVHRIDKDTSGLLMISKKRSALKVLQQHLVDKTI
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                                     RYTLASGERRVKVDAQDPQTKESQTDIVVHGRFT
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CDS             313900..314607       /locus-tag="Psyc-0258"
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                                     YPQASAEQKLLIQQSYADYYIANS
                                     QRTPFFAPIENMLQTLQQQNRRLAVATGKKRKGL
                                     DRVLDASDSHHYFVMTRCADEAGS
                                     KPDPQMLTDILQCTEQQVSDAVFIGDSIYDIQMA
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                                     PTYQVDTPQALAELLCA"
gene            complement(314697..3156 /locus-tag="Psyc-0259"
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CDS             complement(314697..3156 /locus-tag="Psyc-0259"
                05)
                                     /note="GTP-binding domain"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="cell division checkpoint
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                                     ALTNQRQLARSSKTPGRTQMINFFNVGDADRRLV
                                     DLPGYGYAAVPLEMKKEWQVELEE
                                     YLVSRSSLAGLVLMTDIRHPLKFFDEQMLRWAKD
                                     GELPVHILLTKADKLKYGASKNAL
                                     LNTRKRLKQLGLNCSIQLFSALRKEGLDELAGVM
                                     GNWYEYQLEANKIIESSFALLEGS
                                     ELEDAIEKDAVQKDKNLKDSAQKESK"
gene            315892..316227       /gene="scyA"
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CDS             315892..316227       /gene="scyA"
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                                     /note="Signal predicted by SignalP
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                                     1.000) with cleavage site
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                                     /transl-table=11
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                                     class I"
                                     /protein-id="AAZ18130.1"
                                     /db-xref="GI:71037822"
                                     /translation="MLSMTMIFAKSNRFLVSSVS
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                                     CAACHDSGALNAIKKGDSVKWQQLIKQKGMSALI
                                     SSVKNGMIQMPAGGLCEACSNDDY
                                     RKLIEYMSK"
gene            316570..317238       /gene="cc4"
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CDS             316570..317238       /gene="cc4"
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                                     2.0 HMM (Signal peptide probabilty
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                                     probability 0.999 at residue 20"
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                                     c4"
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                                     VDGVSPVPAQPNLGGQNVKYLYKQLVNFKAGYRK
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                                     SQKPWGVAFGNPATTQEATKLFLGGDKSRGVIGC
                                     AGCHGPDAAGNVWAAFPRLGGQHA
                                     EYIATQLKLFRAAGRVDDIDSDDQKRVNDGAKEG
                                     EMGMMQTVASKLSDRDIRILSDYV SAIH"
gene            317468..318610       /locus-tag="Psyc-0262"
CDS             317468..318610       /locus-tag="Psyc-0262"
                                     /note="Possible Na+ dependent
                                     transporter of the SNF family.
                                     Signal peptide and 11
                                     transmembrane helices predicted."
                                     /codon-start=1
                                     /transl-table=11
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                                     TGILTALTELNSAPEVPSFAIAAGLMVIAALLSL
                                     LGVSPLPIGLGLMLIGLIFGVANG
                                     LPNITFAMTNISLGEWARAVALALVSVGAGTGLY
                                     WFGQNRITKQAVTAVGVDNHHAQN
                                     PSRPQASSEYRATKLVLPIWILQLLVGVVALFIS
                                     GMTLPPIGQLLYWAGVIFVASYLI
                                     HYSTQQLAHRFGLLLSLAITSIIALLLVVAIPTV
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gene            318598..319002       /locus-tag="Psyc-0263"
CDS             318598..319002       /locus-tag="Psyc-0263"
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gene            complement(319028..3194 /gene="omlA"
                44)
                                     /locus-tag="Psyc-0264"
                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     0.766) with cleavage site
                                     probability 0.461 at residue 43"
CDS             complement(319028..3194 /gene="omlA"
                44)
                                     /locus-tag="Psyc-0264"
                                     /function="possibly involved in
                                     maintaining the structural
                                     integrity of the cell envelope"
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gene            319768..320202       /gene="fur"
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CDS             319768..320202       /gene="fur"
                                     /locus-tag="Psyc-0265"
                                     /function="The Ferric uptake
                                     regulator or FUR family includes
                                     metal ion uptake regulator
                                     proteins, which bind to the
                                     operator DNA and control the
                                     transcription of metal
                                     ion-responsive genes."
                                     /codon-start=1
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                                     family"
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                                     AETGHLVFATLHANNANQAIDRIIHFFEASRHNQ
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                                     GRRAAIEILLNSQLISDHIRKGDVHEIKDVMTRS
                                     RDSGMQTFDQALFDLYENGEITYK
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gene            complement(321690..3227 /gene="pilT"
                42)
                                     /locus-tag="Psyc-0267"
CDS             complement(321690..3227 /gene="pilT"
                42)
                                     /locus-tag="Psyc-0267"
                                     /function="Pilus retraction
                                     protein: required for twitching
                                     motility and social gliding.
                                     Protein involved in type II
                                     secretion."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="pilus retraction protein
                                     PilT"
                                     /protein-id="AAZ18137.1"
                                     /db-xref="GI:71037829"
                                     /translation="MAEQNLRIEDLLRFAVKLKA
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                                     NQRPDGMLPLNVLIQINIDNEDTK
                                     SGCLPEQLPELIIDIKNYKRLQLRGLMIIPAKAN
                                     TNAFKRTKQLFDDIKRTHPELSQW
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gene                 complement(324062..3253 /locus-tag="Psyc-0269"
                     36)
                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     0.996) with cleavage site
                                     probability 0.413 at residue 29"
CDS                  complement(324062..3253 /locus-tag="Psyc-0269"
                     36)
                                     /note="Transporter associated
                                     domain and two CBS domains
                                     present.  RBS found.  Signal
                                     peptide and 4 transmembrane
                                     helices predicted."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="conserved hypothetical
                                     protein"
                                     /protein-id="AAZ18139.1"
                                     /db-xref="GI:71037831"
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                                     LVTSMFVLFADLMPKRLAMSNAEPIAVKMVRPMI
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                                     GVSTVRQDEMTSEDIYAVMDAGAEAGVIKHQEHH
                                     LIENIFEMQERTVTSVMNPREHIV
                                     YFDTKASTEQVVAVMIKQPHNKFLVCNDDDLEHI
                                     IGYVESRSFLASVLEQQEVCLTDK
                                     ALLKPALFIPDTLSLFEVLETFKSTGADFAVIVN
                                     EYALVVGVITLKDVMSIVMGELVT
                                     LEEQPIVQRTDNSWLIDGMTPIEDVIRSLGMVNL
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gene                 complement(325581..3272 /gene="nadE"
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CDS                  complement(325581..3272 /gene="nadE"
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                                     /EC-number="6.3.5.1"
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                                     /transl-table=11
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                                     (glutamine-hydrolyzing) NAD(+)
                                     synthetase"
                                     /protein-id="AAZ18140.1"
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                                     DIVMIVGYPHVDHHGTFNSAAILHNGHQKGFYHK
                                     QILPNYGVFDERRYFDKGRNQVLF
                                     DYKGITIGLLICEDLWGKGPIAELKKQGADLIVS
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                                     NNLPIVYLNAVGGQDDLVFDGGSMAIQADGSVAH
                                     EASRFMNQLLLASFDVKTAKFDIQ
                                     AKAPLSLSRESEMYQALVVGLRDYVNLSGFTGII
                                     VGLSGGIDSALTLCIAVDALGADK
                                     VYAVMMPYEYTSQISLEDAQAQARRLNVSYTVCP
                                     IFDAVEGIRHTLAPLFNKSPADTT
                                     EENIQARARGVVLMALSNKFGHLVITTGNKSELA
                                     VGYSTLYGDMAGGFDVLKDVYKSQ
                                     VYKLASYRNRLEDTPVIPERVITRPPSAELRPDQ
                                     KDQDSLPDYDVLDGILMSYIDEDM
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CDS                  328065..329204  /locus-tag="Psyc-0271"
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                                     RIKAGYLDVPDSVKDLPVIGQQVKDVLWRVNKNP
                                     AGTLETFRLWVQSHLYYGKIAFDV
                                     VFSSLAKLGMALMTLFFFYRDGTSLVRQIRQALR
                                     NIIGNRIDGYIDSVGTTTRAVVYG
                                     IGLTALAQALLAGIGYYFASAPSPILMTILTFII
                                     ALIPFGTPFVWGSISLFLLSQGHT
                                     VEGIGLALWGILVISWVDNLIRPIVISGATKIPF
                                     IIIFIGVLGGLTAFGFVGLFIGPV
                                     VLAIGLAVWREWISQHKNELFAQQEELAQGKNLI
                                     KVNEPSQDTPL"
gene                 329289..330443  /locus-tag="Psyc-0272"
CDS                  329289..330443  /locus-tag="Psyc-0272"
                                     /function="Pyridoxal (B6)
                                     synthesis"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="probable
                                     erythronate-4-phosphate
                                     dehydrogenase"
                                     /protein-id="AAZ18142.1"
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                                     SLDEFFNPIALGQNTEQQVQVIRV
                                     AGRDINAQLLADLQPDVLLIRSVTQIDQALLANN
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                                     NITFANATGCSKHSVAQYVVSAILTLRPQYWAQS
                                     MTPLTLGIIGLGNIGSTLAQYASD
                                     LGWQVLGYDPLLATSDINNASLEQVLCQSDIVSL
                                     HVPLTDKKDTDTQGAMSISNNFSD
                                     YPTRHLINAETLARMSPHTMLINSARGPVIDAAA
                                     LEADIDATERQVVLDVFEHEPQIA
                                     ESLLSKLAIATPHIAGYTLEGKLRGTQIIYDALC
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gene            330504..331532       /gene="lysS/U"
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CDS             330504..331532       /gene="lysS/U"
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                                     /EC-number="6.1.1.6"
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                                     /protein-id="AAZ18143.1"
                                     /db-xref="GI:71037835"
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                                     VFRDNEIGARHNIEFTMLEWYQPNYSLDDMAAEL
                                     GELLEMLYGYPIIMSHYRYVDAFM
                                     DFVGIHPLTASLSALQAVGEDKGLTGFDFNSAQS
                                     CAIDSEQDRRQSWLDLLFSHAVEP
                                     NLGHDLPTLIIEYPPATAALAKTAVDKDGNKVAK
                                     RFELYIKGIEIANAYDELADGQAL
                                     RERFEQDNQLRKRHNLPQMPIDEHLLAASDDLIP
                                     CSGIAVGVDRLLMVITGAIGLEEV IPFSSGLA"
gene            complement(331821..3322 /locus-tag="Psyc-0274"
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CDS             complement(331821..3322 /locus-tag="Psyc-0274"
                70)
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                                     KKAFADGLNKLVR"
gene            complement(332270..3336 /gene="purK"
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CDS             complement(332270..3336 /gene="purK"
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                                     /locus-tag="Psyc-0275"
                                     /EC-number="4.1.1.21"
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                                     /db-xref="GI:71037837"
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                                     TPTATVEQLANLSKSGKKQGMFPP
                                     TIALDIAQDRLKEKQMFNTLDIATVPFMPVSSEA
                                     ELQQACHELGLPVVLKTSRGGYDG
                                     KGQFVIKADSDIKAAWQELKDAVTGKGSLTQTPA
                                     PLIAEGFIHFSRELSIIAARGQNG
                                     QVRCYDLVENHHHQGILAKTQAPAIGTSHLFKQA
                                     TDAITKVMNHLDYVGVMALELFVT
                                     KDARGNDTLLANEIAPRVHNSGHWSIEGAVTSQF
                                     ENHIRAVVNLPLGDTDNVHPAIMI
                                     NILGQYPDISAVLNIDGVHYHSYHKAERNDRKIA
                                     HITLMPNDVADLEPALAKLVAILP
                                     NKVGLDKKVTPINNPTTAEDSLTTAEVETNAENK
                                     KSSANNDNEQQIAELANPKVEKAK K"
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gene            complement(333860..3344 /gene="purE"
                20)
                                        /locus-tag="Psyc-0276"
CDS             complement(333860..3344 /gene="purE"
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                                        /locus-tag="Psyc-0276"
                                        /EC-number="4.1.1.21"
                                        /function="'de novo' Purine
                                        biosynthesis"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="phosphoribosylaminoimida
                                        zole carboxylase, catalytic
                                        subunit"
                                        /protein-id="AAZ18146.1"
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                                        LLADFDIAFECEVVSAHRTPDRLFDYAKSAKGNG
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                                        PVFGVPVKSSMLSGWDSLLSIVQMPKGVAVGTLA
                                        IGSAGAYNAALLAIQVLALHDESI
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gene            complement(334660..3356 /locus-tag="Psyc-0277"
                31)
CDS             complement(334660..3356 /locus-tag="Psyc-0277"
                31)
                                        /note="Possible protein
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                                        /codon-start=1
                                        /transl-table=11
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                                        protein"
                                        /protein-id="AAZ18147.1"
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                                        TRQHETFLAEVPFGSETHQYWLQRLYEIPLWLEI
                                        DYACFVHACWDVDSMAVLQPLLTE
                                        NNCLTAHGLIATSREGTVAFDALERVLKGVETPL
                                        PNGLVMVDKEGTKRTRVRVRWWLD
                                        ALNTRSIHEVARAPLSALAQIPKDALAENIDFTL
                                        KTHKPVFVGHYWLTGEPEPLSPQV
                                        ICTDYSAAVDSGYLTCYQLDSEQPLPLKTSHFIQ
                                        YRHDQDTNILGSI"
gene            complement(335859..3364 /locus-tag="Psyc-0278"
                67)
                                        /note="Signal predicted by SignalP
                                        2.0 HMM (Signal peptide probabilty
                                        0.663) with cleavage site
                                        probability 0.427 at residue 20"
CDS             complement(335859..3364 /locus-tag="Psyc-0278"
                67)
                                        /function="peptidase activity"
                                        /note="6 transmembrane domains"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="possible Rhomboid family
                                        protein"
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                                        QNKALFNRLIFYPPAVNNGQWDRF
                                        VTHGFIHADSMHLLFNMFTLYFFGRAIEGLYQKF
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                                        HKQSASYLSLGASGGVSAVLFAFILLAPWEKIYL
                                        FAIIPIPAILFAVAYVAYSIYSDK
                                        RGGSNINHMAHMWGGAFGVIATIILEPQVLPHFL
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CDS             336924..338426          /locus-tag="Psyc-0279"
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                                        PLAYQELKILANGQFLPAFLQGEQASLRPYLPIW
                                        SAPIIGALQHPDDELFQSQRVLAG
                                        TVIPAVALNNYEPAAVDIITSPSFTAESPIPTLD
                                        ERLSTDSIHVSPAEHHLAENTSLR
                                        REKTRTRNQRNDMLLWTFVLLGAVTAIGLVWALL
                                        IKPNDTPPVEAVVTTPVVVPPVIE
                                        PPVQVVTPIELIVGVDNNGSLYTCSGSVGDVALQ
                                        SLLQQALNTSFGEQAGMCQLIVKE
                                        GVASSVANMPIEVLPNVLTLLRSVPFARLQLQND
                                        RITVEAPDTMQLQRLMADMRTLLP
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                                        NNQFENAPANNSANNVEYQAPDDE
                                        TNDSVMPALARNNNTNNFNSAPSGSNGSVSSSEF
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gene            338964..340565          /locus-tag="Psyc-0280"
CDS             338964..340565          /locus-tag="Psyc-0280"
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                                        /protein-id="AAZ18150.1"
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                                        EIKSLSGTTPVPQFLNENIDSYQRHIPVWATAVL
                                        PVGVIAAAPVSTGAHISDTVSTAP
                                        LQHEAEKDGSFMKALLPIIGLIILGALAWALLRG
                                        CQDKPEPVGMPIVTAQQAANSDGQ
                                        AVAANMAPASLRITTGENSELYACRMDVGNDTLQ
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                                        NFSIDMPATAQLATILSIFKNVPNASMLVKGDTI
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                                        RDVARALSLQVVNFEVDKALIPDA
                                        NKALLDRAVKLMEQVPNMTLMIIGHTDKTADAAY
                                        NLKLSEERAQAMKAYLVAQGADPS
                                        KLMTKGMGETDPIADNTTDQGRFRNRRIEFVVYD
                                        ETTTANDGLAISNDALDPDLNPLD
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gene            complement(340828..3419 /locus-tag="Psyc-0281"
                10)
CDS             complement(340828..3419 /locus-tag="Psyc-0281"
                10)
                                        /EC-number="3.2.1.52"
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                                        glycosidic bond between two or
                                        more carbohydrates, or between a
                                        carbohydrate and a
                                        non-carbohydrate moiety."
                                        /codon-start=1
                                        /transl-table=11
                                        /product="glycoside hydrolase
                                        family protein"
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                                     VDNKPAGFSKIWLKDIIREQLNFEGVLFSDDLSM
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gene            342390..344603       /gene="prc"
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CDS             342390..344603       /gene="prc"
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                                     /function="Proteolysis and
                                     peptidolysis: serine-type
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                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     0.994) with cleavage site
                                     probability 0.884 at residue 33"
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                                     SLDEVAKMLGFFIKSGPLVQIRDNRGNIQVYRDD
                                     DGGEQLYDGKVVVLTNLASASASE
                                     IFAAAIQDYGRGLVVGSTTTGKGSAQIQLDSLAL
                                     GSATLTQRKFYRITGGSTQNKGVV
                                     PDVELVNIYDNATFGERAQKKALPWDTIKTAPYK
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                                     PQFVYLSTLNDIRNMEDEKKPVALDINKRRAKMQ
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                                     EAAYIMLSTEPKTLSSPEEKP"
gene            complement(345101..3455 /gene="slyD"
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CDS             complement(345101..3455 /gene="slyD"
                86)
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CDS             346048..348033       /locus-tag="Psyc-0284"
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                                     WVKTVRPDVMLEVDLRREAFTPLLWVFEGFTSYI
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                                     NRYYQTPGRAQQSVAESSFDAWIKLYRNDENTGN
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                                     LPIEKLLAANGIQFYTNNKETADKHVPWGMRCTE
                                     TPAGIKINRVTRGSAAAKAGLSAH
                                     DVIIAIDGIKADNKQLALFNDASHDIECHLFRRD
                                     ELMMVKVLPRVLNDNTHAKNSLEK
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gene            complement(348127..3489 /locus-tag="Psyc-0285"
                66)
                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     0.996) with cleavage site
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CDS             complement(348127..3489 /locus-tag="Psyc-0285"
                66)
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                                     GMLGHHHGAVDMAKIALKYGTDKEMRQLAKDIID
                                     SQQLEIDIMNKWLASHPDAPKPKP
                                     NTQAMQQAYAAGMQTMHNNMMAGIADPIPDMAFA
                                     RGMLPHHRGAVDMAKIQLQYGTDE
                                     EMRKLAQDIIDAQQPEIVLLQEWIAKMLVNAEKD
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gene            complement(349170..3497 /gene="rsu"
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CDS             complement(349170..3497 /gene="rsu"
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                                     /EC-number="5.4.99.-"
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                                     modification"
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                                     /protein-id="AAZ18156.1"
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gene            complement(350508..3527 /gene="icd2"
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                                     KGDIWRMCQVKDEPIQDWVKLAVRRARESNTPVI
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                                     DTTGLHIEIMSQVRAMRYTLERVARGLDTISATG
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                                     DSLGEFLALTVSLEHLAQNDGNAK
                                     AQVLADTLDTATEKLLLDDKSPSRKTGELDNRGS
                                     HFYLAMYWAQELAAQDKDSELKAQ
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CDS             353534..354886       /locus-tag="Psyc-0288"
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                                     QFLWQNKNLSQNDQLFADFEEFLATLKAKKRKTI
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                                     MAEHVMLAQALDAGGEIIASSLFL
                                     YDKPDNKMATLYGRYWGALGEYDSLHFELCYYQG
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gene            354939..355445       /gene="ubiC"
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                                    ARRLQQLKSTPIGYVLFKRSRTLPNQRFIKHTVD
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gene            355846..357102      /gene="glyA"
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CDS             355846..357102      /gene="glyA"
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                                    /EC-number="2.1.2.1"
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                                    and biosynthesis, Lysine
                                    degradation"
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                                    /product="serine
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                                    AVFLALLEANDTVLGMSLDAGGHLTHGAHINFSG
                                    LNYNAVQYGLVEGTGLIDYDQVES
                                    LAKEHKPKMIIAGFSAYSQVVDWARFREIADEVG
                                    AYLLVDMAHVAGLIAGGVYPSPVP
                                    FADVVTTTTHKTLRGPRSGMILARDEKLAKKLNS
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                                    ALENNFKTYQQQVVKNAQAMAKVIQERGYEIISG
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gene            complement(357352..3577 /locus-tag="Psyc-0291"
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CDS             complement(357352..3577 /locus-tag="Psyc-0291"
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gene            complement(357728..3584 /locus-tag="Psyc-0292"
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CDS             complement(357728..3584 /locus-tag="Psyc-0292"
                71)
                                    /function="RNA binding
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                                    /note="Citation: Nucleic Acids
                                    Res. 1992 Jun 11;20(11):2861-4."
                                    /codon-start=1
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                                     a cold-shock DNA-binding domain"
                                     /protein-id="AAZ18162.1"
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                                     QNKKSSLSTLFSLIAIIAVAVYFFADIKSSFFAD
                                     STPPATLTQNSIETASTANAVAIT
                                     GDAQIDQTIALIQQGGPFSYPNKDGTKFYNREGK
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                                     RRIVTGGHPPTIYYLTLDHYDSFQKLEVK"
gene            complement(358637..3599 /gene="proA"
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CDS             complement(358637..3599 /gene="proA"
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                                     /locus-tag="Psyc-0293"
                                     /EC-number="1.2.1.41"
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                                     EVTDMTYRPSGIHLGKMRVPLGVVGMIYESRPNV
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                                     ESNQAIAKCILEGLKKVGMSEYSVQVLETTDRAA
                                     VGELITMTDYVDVIVPRGGKGLIE
                                     RISRDARVPVIKHLDGNCHTFIDSDADPEIAIKV
                                     SVNAKTHRYGTCNTMETLLVDEAI
                                     ANELLPKIAEAIVKADDAMQLRLDDKAQAILNDN
                                     TTLKGHLSAATAEDWDTEYLAPIL
                                     AIKILSGIDEAIEHINTHGSHHTDVIITDNYTKS
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gene            360599..361396       /locus-tag="Psyc-0294"
CDS             360599..361396       /locus-tag="Psyc-0294"
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                                     /product="ABC basic amino acid
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                                     /protein-id="AAZ18164.1"
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                                     GFVFQNFNLWPHKTIIDNIIEGPIQVLKIKKDQA
                                     ISDAEKLLDKVGLLDKKDAYPANL
                                     SGGQRQRVAIARALAMQPQVLLFDEPTSALDPEL
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                                     MRFAREVSSKVVFLHQGVIEEIGTPEQVFDNPKS
                                     ERVKDFMASHRQN"
gene            361873..362673       /locus-tag="Psyc-0295"
CDS             361873..362673       /locus-tag="Psyc-0295"
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                                     2.0 HMM (Signal peptide probabilty
                                     0.998) with cleavage site
                                     probability 0.394 at residue 25"
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                                     protein"
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                                    TDTKGSFDPKVIKNLTLGGQRSTT
                                    PGAYLQDNYEGKDGNTVKLYDSYDNAYLDLKSGR
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gene            362760..363689      /locus-tag="Psyc-0296"
CDS             362760..363689      /locus-tag="Psyc-0296"
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                                    0.968) with cleavage site
                                    probability 0.651 at residue 34"
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                                    IILIGKKGDDVSVDALKGQPIASQ
                                    RSTVASQYLQDKHADADIKLYDTQDNAYLDLTSG
                                    RVRAMMSDKVTGIDWLKTEAGKDY
                                    EVKGQEISTSDDAMGIAFRKGDPLVAKFNKALAE
                                    LKDNGTYDQITGSYFGTSSTTAAQ
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gene            364285..365019      /locus-tag="Psyc-0297"
CDS             364285..365019      /locus-tag="Psyc-0297"
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                                    subunit"
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                                    LSIAFGAYATEIFRMSIQEIPIGQQEAAQAIGMR
                                    PFQTFYRITLPQVWQIALPGLGNL
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gene            365033..365758      /locus-tag="Psyc-0298"
CDS             365033..365758      /locus-tag="Psyc-0298"
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                                    subunit"
                                    /protein-id="AAZ18168.1"
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                                    MSKWQKLTRITLPRAFGIVIPVYS
                                    NEVIFMLKGSALASTIALMDITGVARTISARTYT
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                                    DFKNVEYQFYINNELKQNGDSALMLFPVYELLVD
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gene            366970..369171      /locus-tag="Psyc-0300"
CDS             366970..369171      /locus-tag="Psyc-0300"
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                                    RPEWVSVSPMTGEVYVTLTNNKYRGVRDDQPVSA
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CDS             369539..371005      /locus-tag="Psyc-0301"
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gene            372590..373549           /gene="gltI"
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CDS             372590..373549           /gene="gltI"
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CDS             373659..374405           /gene="gltJ"
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gene            374402..375073       /gene="gltK"
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CDS             376375..377634       /locus-tag="Psyc-0307"
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CDS 379861..381471
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CDS 381521..382327
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metabolism, Tryptophan metabolism"
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                                     AQGIKVRGVISCTVGCPYEGEIDP
                                     SQVAYVTKRLVEIGSEQIGIADTIGVGTPLKVQR
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CDS             385592..386779       /gene="acd"
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                                     LGGYIFPSIYLQRESLFSGTKQIT
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                                     /function="Attaches biotin to
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                                     /product="probable biotin-(acetyl
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CDS             388969..389292  /locus-tag="Psyc-0316"
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                                essential for successful
                                chromosome transmission during
                                replication and segregation of the
                                genome."
                                /note="Citation: Hirano T. 1998.
                                SMC protein complexes and
                                higher-order chromosome dynamics.
                                Curr Opin Cell Biol. 10:317-322."
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                                     a cofactor."
                                     /note="This protein also contains
                                     a BRCT domain (predominantly in
                                     proteins involved in cell cycle
                                     checkpoint functions responsive to
                                     DNA damage).; Citation: Lee JY,
                                     Chang C, Song HK, Moon J, Yang JK,
                                     Kim HK, Kwon ST, Suh SW. 2000.
                                     Crystal structure of
                                     NAD(+)-dependent DNA ligase:
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                                     functional implications. EMBO J.
                                     19:1119-1129."
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                                     /translation="MQLSLEKLPVSERMVLIEQL
                                     WDSIISDSKSLKDIERITLTSSQE
                                     KLVELLDKRLSEYAENKFYHRFEMEKMMGSRGIQ
                                     ILCHFTPINNLESILNNGLYPRDY
                                     IDENLPDAIWTDDGRFEGMKNGVCLSISFPNHQM
                                     FYRKRMQLKDIESWAVIVLDARKV
                                     ILNHDCAFFQTNSAFGDYRNKSLSEFMTSNAFFS
                                     LFEEKVETRNGVVTRQDYLTDEFP
                                     TDVQAEVVVFDHIPPDSIEACYLQSEKYLKYFEE
                                     KFSKFTFIEDSNDNSAFGKRE"
gene            complement(400165..4006 /locus-tag="Psyc-0323"
                95)
                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     0.976) with cleavage site
                                     probability 0.639 at residue 26"
CDS             complement(400165..4006 /locus-tag="Psyc-0323"
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                95)
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                                     /db-xref="GI:71037884"
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                                     GCDNSADTAAKKTDAAVSTADSAA
                                     ANTIDWSVMDSGEKPADLANYQYPFALDSQNVRD
                                     YAEYFKVDNATAQHNLTVSMASNE
                                     ALSKALDQLSESYVSHELTDDKDMKLIIHTTPDI
                                     AAGSYDYVLAGEFAKGLVLPIVIV
                                     PDGKKSEAKAHGEMVE"
gene            complement(401246..4036 /locus-tag="Psyc-0324"
                93)
CDS             complement(401246..4036 /locus-tag="Psyc-0324"
                93)
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                                     /db-xref="GI:71037885"
                                     /translation="MSADTIARTAFKQGTKPLYD
                                     YDKHWASCYEPAPYLPMSRKEMDE
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                                     GFRVGIIAQPDWKSKDAFMELGKP
                                     VYAYGVTAGNMDSMINRYTADRKIRSDDAYSPGN
                                     VADKRPDRAAIVYSQRCREAYPDV
                                     PIILGGIEGSLRRIAHYDYWSDKVRRSILLDARA
                                     DVLLYGNAERAIVDVVHGLSKGYS
                                     FEQMSNLRGTAYLLTPTRRHWQAGMTEVASNDVD
                                     TVGRVDPIINPYVMTEDLDLCSIE
                                     QDKPSDSPVGQALSGMSGQYPGFVSEPVTNKILN
                                     TDQVDEETQVVQMRGFNKPMTARK
                                     HKIKMPPREQTVIRLPDYEHVKSDPVLYAHASRI
                                     LHLETNPGNARALVQRHSSGAGNS
                                     HTSIDVWLNPPPIPLSTEEMDYVFDLPYARLPHP
                                     SYGDARIPAYDMIKFSVNIMRGCF
                                     GGCTFCSITEHEGRIIQNRSEESILREVEAIRDT
                                     APNFTGVISDLGGPTANMYRLNCK
                                     DETIEKNCRKPSCVYPDICENLITDHSNLTQLYR
                                     KARDIKGVKKILIASGLRYDLAIK
                                     DPEYVKELVSHHVGGYLKIAPEHSEENVLSKMMK
                                     PGMGNYDKFKAMFEQYSQEAGKEQ
                                     YLIPYFIAAHPGTKDEDMMNLALWLKGNGYRADQ
                                     VQAFYPSPMATATTMYHTHKDPLH
                                     KISRDEGDVDIVKSGKQRKLHKAFLRYHDPKNWV
                                     MLRKALQDMGRGDLIGKNRGCLIP
                                     PFNASLEGRDAAQDSYQSARKKNSRLGNDSVKRS
                                     NKSADSWSNKGTAGKSASSKKNVS
                                     KGNFQTQHTGLPPRKTK"
gene            complement(404366..4048 /gene="smpB"
                42)
                                     /locus-tag="Psyc-0325"
CDS             complement(404366..4048 /gene="smpB"
                42)
                                     /locus-tag="Psyc-0325"
                                     /function="recognizes stalled
                                     ribosomes such as occur during
                                     translation from message that
                                     lacks a stop codon."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="SsrA-binding protein"
                                     /protein-id="AAZ18194.1"
                                     /db-xref="GI:71037886"
                                     /translation="MSKKSKKPENQICANKKARH
                                     EYFIEETFEAGLSLQGWEVKAIRA
                                     GKMTITEAYIIFRNNEAFLFGAHIQPLLSSSTHV
                                     SPDSIRTRKLLLNRREIEKLFGAV
                                     NQKGYACVPLSCYWKNSLVKCQIGLALGKKQHDK
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                                     RKTLKDRDWERDKQRGFKKDLD"
gene            405107..405619       /gene="coaD"
                                     /locus-tag="Psyc-0326"
CDS             405107..405619       /gene="coaD"
                                     /locus-tag="Psyc-0326"
                                     /EC-number="2.7.7.3"
                                     /function="Biosynthesis of
                                     pantothenate and CoA"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="Phosphopantetheine
                                     adenylyltransferase"
                                     /protein-id="AAZ18195.1"
                                     /db-xref="GI:71037887"
                                     /translation="MSSSATSSKLHTKILYPGTF
                                     DPITNGHVDLVTRATKLFDEVVIA
                                     VASGHHKKPLFNFEERVALVETVFIDLPQVSVIG
                                     FEGLLVDFMREKNATAVLRGLRVM
                                     SDFEYEFQLANMNRELDENFEAVFLTPSQNYSFI
                                     SSTMIREIAKLGGDVTKFVPPCVS
                                     EAFIQKLGSK"
gene            405692..405940       /locus-tag="Psyc-0327"
CDS             405692..405940       /locus-tag="Psyc-0327"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="putative 4Fe-4S
                                     ferredoxin"
                                     /protein-id="AAZ18196.1"
                                     /db-xref="GI:71037888"
                                     /translation="MALLITDECINCDVCEPACP
                                     NEAISEGDDIYVIDPDLCTECVGH
                                     FDEPQCVVICPVDCIPHDPNHVETESDLMSKYKR
                                     ITGK"
gene            405944..407254       /gene="bioA"
                                     /locus-tag="Psyc-0328"
CDS             405944..407254       /gene="bioA"
                                     /locus-tag="Psyc-0328"
                                     /EC-number="2.6.1.-"
                                     /function="Biotin synthesis"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="aminotransferase"
                                     /protein-id="AAZ18197.1"
                                     /db-xref="GI:71037889"
                                     /translation="MTTVSTNDFDQQHLWHPYAS
                                     LPPRYPNIMIDHADGIHIVTQDGT
                                     RLIDGMSSWWASVHGYNHPKLNAAIIEQLGKMAH
                                     VMFGGLTHQPAIDLGKKLLSIVPA
                                     GIDAIFYADSGSIAVEVALKMALQYQIAAKRPNK
                                     QQFASTHSGYYGDTWHAMSVCDPI
                                     NGMHSLYGKQLPMQHFVAAPPMGFERDITQNERD
                                     ELTAFFAKNSHQLAGFIIEPIIQG
                                     AGGMRFYSPEYLQLLRQLCCEHDVLLIADEIATG
                                     FGRSGKLFACEHANISPDIMTIGK
                                     ALTGGYMTFAATLCTRSIADTISQSDYSALMHGP
                                     TFMGNPLACAVACASIDLILSYDI
                                     EARTENMHALMVEQLASAAKLEGVKEVRCLGAVA
                                     VIELDDAVDMPTFQSLLIEHGIWV
                                     RPFGKLVYIMPPYIITDSELITLCQALLKVVSIY
                                     LTQTSLSAKG"
gene            407266..407985       /gene="bioD"
                                     /locus-tag="Psyc-0329"
CDS             407266..407985       /gene="bioD"
                                     /locus-tag="Psyc-0329"
                                     /EC-number="6.3.3.3"
                                     /function="Biotin synthesis"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="dethiobiotin synthase"
                                     /protein-id="AAZ18198.1"
                                     /db-xref="GI:71037890"
                                     /translation="MSVLFISGIDTDIGKTYATG
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                                     MIAKVLMQQGINVITQKLVQTGVA
                                     RDLSSGKMGVADDIITHRQLMGIPLQPCDVDNTT
                                     CPYRFEKPASPHLSARLASDILNP
                                     DVITSATKSLQADYEVVLLEGAGGLLVPITEKLL
                                     TLDYIAQEGYPVILVTSGRLGSIN
                                     HTLLSLEAITSRGLEVHSIVYNHIHDSAAQTDAE
                                     IAAGTIEFLQKYLAQYYPTAHWLS
                                     LPVQDNDGFNNIDYILPQNFI"
gene            408102..408403       /locus-tag="Psyc-R0010"
misc-RNA        408102..408403       /locus-tag="Psyc-R0010"
                                     /product="RNA component of RNaseP"
gene            408595..408671       /locus-tag="Psyc-R0011"
tRNA            408595..408671       /locus-tag="Psyc-R0011"
                                     /product="tRNA-Met"
gene            409080..410876       /gene="lepA"
                                     /locus-tag="Psyc-0330"
CDS             409080..410876       /gene="lepA"
                                     /locus-tag="Psyc-0330"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="GTP-binding protein
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                                     /protein-id="AAZ18199.1"
                                     /db-xref="GI:71037891"
                                     /translation="MTALANIRNFSIIAHIDHGK
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                                     DSMDIERERGITIKAQSVTLYYDHPNGERYQLNF
                                     IDTPGHVDFSYEVSRSLAACEGAL
                                     LVVDAAQGVEAQSVANCYTAVDQGLEVMAVLNKI
                                     DLPQVEPERVIQEIEDIIGIDAVD
                                     APRVSAKSGLGVDKLLEALVEFIPAPTGDRDAPL
                                     QALIIDSWFDNYLGVVSLVRVRQG
                                     TIKKGDKLYIKSTKDAHLVGSIGVFTPKPLDTGI
                                     LEAGEVGFIIAGIKDIAGAPVGDT
                                     ITHASTPDVDCIPGFKQITPQVYAGMFPVESTDF
                                     EKFREALQKLQINDASLFFEPDTS
                                     DALGFGFRCGFLGMLHMEIIQERLEREYDLDLIT
                                     TAPSVIYEIVKKDGSIIYVDNPSR
                                     LPEPNNIEEFREPIARCQILVPQDYLGNVMTLCI
                                     ERRGVQVDMRFMGRQVQLIFDIPM
                                     GEVVMDFFDRLKSVSRGFASLDYNFERYQVDKLV
                                     KVDVLINGDKVDALAMIVHETQSR
                                     YRGNALVSKMKELIPRQMFDVAIQAAIGSQIIGR
                                     STVKAMRKDVLAKCYGGDVSRKKK
                                     LLSKQKAGKKRMKQVGNVEIPQEAFLAVLQVD"
gene            410955..411857       /gene="lepB"
                                     /locus-tag="Psyc-0331"
CDS             410955..411857       /gene="lepB"
                                     /locus-tag="Psyc-0331"
                                     /EC-number="3.4.21.89"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="signal peptidase I.
                                     Serine peptidase. MEROPS family
                                     S26A"
                                     /protein-id="AAZ18200.1"
                                     /db-xref="GI:71037892"
                                     /translation="MDFDFNLILVPLTIGLGLIW
                                     LLDKLTLKQRKTRGRGKESWLVRW
                                     AYDFFPVLAVVLIVRSFLIEPFNIPSSSMVPTLY
                                     TGDFIAVNKYAYGVRLPLTYNKVI
                                     DTGAPEHGDVAVFRYPENPSIYYIKRVIGLPGDT
                                     VSYNQGTLAINDVPVATQAMDFDA
                                     NAELTSQLYSAGQVAPGQMLTEENAAAMGQQEEG
                                     DAQYFKETQGKHEYVVRYLNGMNS
                                     SQYAPFLQQQSPEVVSSEGNEWRINVPEGQYFVM
                                     GDNRDRSADGRFWGFVPDDNLAGK
                                     AVYIWMHKPPGLQLPTFKRNGAID"
gene            412018..412413       /locus-tag="Psyc-0332"
CDS             412018..412413       /locus-tag="Psyc-0332"
                                     /note="One transmembrane helix
                                     predicted."
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                                    /codon-start=1
                                    /transl-table=11
                                    /product="hypothetical protein"
                                    /protein-id="AAZ18201.1"
                                    /db-xref="GI:71037893"
                                    /translation="MVQQLSGLSTQRGASVTSIV
                                    FIIIALGVAAKLIVAIVPAQIADY
                                    QLTKTLGAQLQESNSKKETAKQFVVRVDKQLSIN
                                    ADYDTKAEEIFTFKDKKTGQLAIY
                                    KKYEKTHTLFGNIDIVNRFEGDIDPTIAD"
gene            412567..413364      /gene="rnc"
                                    /locus-tag="Psyc-0333"
CDS             412567..413364      /gene="rnc"
                                    /locus-tag="Psyc-0333"
                                    /EC-number="3.1.26.3"
                                    /note="contains dsRNA binding
                                    domain at c- terminus and
                                    ribonuclease 3 domain"
                                    /codon-start=1
                                    /transl-table=11
                                    /product="RNAse III"
                                    /protein-id="AAZ18202.1"
                                    /db-xref="GI:71037894"
                                    /translation="MKPTSQYPQAVPNPPKNSLS
                                    DDTLVISSEFIQRLAVLTRKLGYV
                                    FNDLSLAKLALTHRSFDSKKNYERLEFLGDALLG
                                    MIVGEALYHRYPTQNEGRLTRMRA
                                    TLVRQESLVIIAQNLELSNQLILGVGERKGGGRN
                                    RASILADAVESLIGAIYLDSQDMN
                                    ITRECVLSWYGDLIDNVNDQKALKDAKSRLQEWL
                                    QSKQFDLPHYELMETRGNAPHQLF
                                    VVRCQVNIINCPDITESGESRRIAEQKAAELMIN
                                    QLHKLPGVPKKRR"
gene            413679..414671      /gene="era"
                                    /locus-tag="Psyc-0334"
CDS             413679..414671      /gene="era"
                                    /locus-tag="Psyc-0334"
                                    /function="Involved in cell growth
                                    (cell division), with a function
                                    of GTP binding."
                                    /codon-start=1
                                    /transl-table=11
                                    /product="probable GTP-binding
                                    protein Era"
                                    /protein-id="AAZ18203.1"
                                    /db-xref="GI:71037895"
                                    /translation="MENDTVDNDSAIEAFFSPDN
                                    SKLAVEGFKTGYVAIVGRPNVGKS
                                    TLMNHLLGQKLSITSRKPQTTRHRIHGILSNDEM
                                    QAVFVDTPGIHRNEVRAINERMNK
                                    AAVSALVDVDLVLFVVDSDQWRDDDLLVLQKLGD
                                    TNLNVVLVINKADTLKDKGSVLPL
                                    METFNDSFDFADIVPVSALKNQNLDRLQEVIASH
                                    LPVAAPIYDTEQITDRSERFLASE
                                    IIREKIMRSAGDEVPYDLTVQIDGFKDEAAHTDP
                                    KTGRPRKACTFIDATIYVERSGQK
                                    AIVIGDKGQRIKQVGMDARKDMEQLFDKKIMLTL
                                    WVKVKRGWSDDERALTSLGY"
gene            414720..415484      /gene="recO"
                                    /locus-tag="Psyc-0335"
CDS             414720..415484      /gene="recO"
                                    /locus-tag="Psyc-0335"
                                    /function="Involved in RecF
                                    pathway of recombination."
                                    /codon-start=1
                                    /transl-table=11
                                    /product="DNA replication and
                                    repair protein RecO"
                                    /protein-id="AAZ18204.1"
                                    /db-xref="GI:71037896"
                                    /translation="MRNEALIGYLLHQRPYQEKR
                                    ALYYLFSQQHGVIHGIGKKGAPLF
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                                     MPLQLFATGKRDLKTFSQINIASFISAHQSAPQN
                                     DDAANAETRYQESITGQHQYAALY
                                     LNEILWRLLPTEDPMPILWQHYQDSLYKLKKPLS
                                     ADELRLCLRHFESYLFNELGFSLT
                                     LNQDSLENPIDSAQVYRFLPDVGLMPIVHHEDSE
                                     SLVRHTVFNGSEVLMMLEQGLSVN
                                     TLNMWSRLHRQLIDHLLDYQPLQSRLLWQQQQRY
                                     QL"
gene                 415584..416378  /gene="pdxJ"
                                     /locus-tag="Psyc-0336"
CDS                  415584..416378  /gene="pdxJ"
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                                     /function="B6 synthesis"
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                                     /product="putative pyridoxal
                                     phosphate biosynthetic protein"
                                     /protein-id="AAZ18205.1"
                                     /db-xref="GI:71037897"
                                     /translation="MTATAQILPNTLEQNSDNIS
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                                     EMAGQLTTRMNLEMAATTEMLEIA
                                     CRVKPYWVCLVPEKRAELTTEGGLDVAGQLDLLK
                                     DYVAKLQAAGIKVSLFIDPEDKQI
                                     NAAVTCGADAIELHTGSYAEAGLAGDIEKGSVEL
                                     ERIKTAVITAKRIDSKLLVNAGHG
                                     LTHDNVNAIAQIDGIYELNIGHALIADALFVGIE
                                     QAVIMMKIAMHR"
gene                 complement(416416..4170
                     03)             /locus-tag="Psyc-0337"
CDS                  complement(416416..4170
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                                     /transl-table=11
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                                     /db-xref="GI:71037898"
                                     /translation="MTISYRTLLICSKDCRRHNE
                                     HGFNLVELIITVAILAIIAMIATP
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                                     NLLVCLSNGGGLCHRDSFKQLLLF
                                     SDKNNNNNNYDVGIDDLLEDQALNPKYSTLYLRVG
                                     NNRHYTKFWGDSGSPRGHFGHIKY
                                     CPTSTYNHTMYQISFSQVGRITYKPHEDHPTGCG
                                     T"
gene                 417594..418778  /gene="oprF"
                                     /locus-tag="Psyc-0338"
CDS                  417594..418778  /gene="oprF"
                                     /locus-tag="Psyc-0338"
                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     1.000) with cleavage site
                                     probability 0.980 at residue 23"
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                                     /transl-table=11
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                                     protein"
                                     /protein-id="AAZ18207.1"
                                     /db-xref="GI:71037899"
                                     /translation="MKLNKIALALFAITAAPLAA
                                     NAGVTISPLLLGYHYSEGADDEQV
                                     ETTSPAGVGDSGFYKENGLYTGAALGIELTPSTQ
                                     FQVEYGVSNTDGVDPASTDSFDAE
                                     QEMISGNFLIGTEQFTGYTDNKLKPYVLVGAGQS
                                     KIKIENAAGTEVAETKDTIGNLGL
                                     GAMYRINDALSLRGEARAIHNFDNNWWEGMALAG
                                     LEVVLGGHLAPAVAVPPMQEPDVQ
                                     TPPIVIVESDLDSDGDGVLDSIDACPGTPMNVVV
                                     DARGCPVPVDITDELKMELRVFFD
                                     NDKSAIKTQYKPEIAKVAEKMREYPNSTARVEGH
                                     ASKTGPSARYNQRLSEARAVAVKS
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                                        MNRRVYAIITGDKTMTVEQTKDMV VQ"
gene            419133..420980          /locus-tag="Psyc-0339"
CDS             419133..420980          /locus-tag="Psyc-0339"
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                                        /product="putative regulatory
                                        protein TypA or elongation factor
                                        Tu"
                                        /protein-id="AAZ18208.1"
                                        /db-xref="GI:71037900"
                                        /translation="MANDIKHLRNIAIIAHVDHG
                                        KTTLVDKLLHQSGTFGDRANIAER
                                        AMDSGDIEQERGITILAKNTAIRWTDNTDGTEYR
                                        INIVDTPGHADFGGEVERVMSMVD
                                        CVLLVVDAVDGPMPQTRFVTQKAFEQGLKPIVVI
                                        NKIDRPGSRPDWVMDQIFDLFDNL
                                        GATDEQLDFPVVYASALNGIAGLEADNLADDMTP
                                        LFKTIVDVVQPPQVDAEAPFRMQI
                                        SSLDYNSFVGVIGIGRIQRGKVKTNTQVTVIDKN
                                        GNTRNGRILKIMGYHGLDRIDVED
                                        AQAGDIVCITGIDALNISDTICDPSTVEALKPLT
                                        VDEPTVSMNFQVNNSPFAGRDGKF
                                        VTSRNIRERLERELIHNVALRVEDTESPDKFKVS
                                        GRGELHLSVLIENMRREGFEMGVS
                                        GPEVIVKEVDGKLQEPYENVVFDIEDEHQGSIME
                                        QIGLRKGEMTNMELDGKGRMRIEA
                                        TMPARGLIGFRSEFLTLTSGSGIMTSSFSHYGPQ
                                        KIGDVGGRSNGVLVSMAKGVCLGF
                                        ALFNLQKRGKLFAEPQLEVYEGMIVGLNSRNDDM
                                        AVNPTTAKQLTNVRASGTDEALTL
                                        TPAVKFTLEQALEFIQDDELVEVTPKAIRLRKRY
                                        LTESERKRYGRKKGA"
gene            421373..421810          /gene="mscL"
                                        /locus-tag="Psyc-0340"
CDS             421373..421810          /gene="mscL"
                                        /locus-tag="Psyc-0340"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="large-conductance
                                        mechanosensitive channel MscL"
                                        /protein-id="AAZ18209.1"
                                        /db-xref="GI:71037901"
                                        /translation="MSMVSEFKKFALKGNVMDLA
                                        VGVIIGGAFATITKSLVEDVIMPI
                                        VAFIAGGEINFKNMFLILGDTPEGVVMTYDALKA
                                        AGVPVLAYGNFITVLINFLILAFI
                                        IFMMVKMVNRLRRADEVVEKIAGPSEEVQLLREI
                                        SAKLGNINK"
gene            complement(421913..4223 /locus-tag="Psyc-0341"
                65)
                                        /note="Signal predicted by SignalP
                                        2.0 HMM (Signal peptide probabilty
                                        1.000) with cleavage site
                                        probability 0.996 at residue 35"
CDS             complement(421913..4223 /locus-tag="Psyc-0341"
                65)
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                                        /transl-table=11
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                                        /db-xref="GI:71037902"
                                        /translation="MTAQANIKCTAKYKLLTVMV
                                        SASLAFASMQSALAAIEIDETDFG
                                        PSYETMAVDTVVGKPLQLIAAVAGTAAYIVSLPF
                                        SLIGGNAEQAQQKLVVEPWNAMSR
                                        CLGCTIAEDNYYKSQVVDNNVDNNVVRIVVDQPS
                                        EIIINTNDHVVVRP"
gene            complement(422692..4236 /gene="fpg"
                21)
                                        /locus-tag="Psyc-0342"
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CDS             complement(422692..4236 /gene="fpg"
                21)
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                                        /EC-number="3.2.2.23"
                                        /function="Formamidopyrimidine-DNA
                                        glycosylase (Fpg) is a DNA repair
                                        enzyme that excises oxidized
                                        purines from damaged DNA (base
                                        excision repair)."
                                        /note="Citation: Gilboa R, Zharkov
                                        DO, Golan G, Fernandes AS,
                                        Gerchman SE, Matz E,   Kycia JH,
                                        Grollman AP, Shoham G. 2002.
                                        Structure of
                                        formamidopyrimidine-DNA
                                        glycosylase covalently complexed
                                        to DNA. J Biol Chem.
                                        277:19811-19816."
                                        /codon-start=1
                                        /transl-table=11
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                                        apyrimidinic site) lyase /
                                        Formamidopyrimidine-DNA
                                        glycosylase"
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                                        /translation="MPELPEVETTKTSLAPLLGQ
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                                        DYTLDSVERRAKYLILNFIPLADDGISSTVQPRN
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                                        KRKHDHLIMSFIGADSTQTQLHYYDPRRFGSILW
                                        LEEYGDKLLNHLGPEPLSDAFTAD
                                        YLYHLIQRSRQSIQTQNSKSIKKQPIKRAIKSVI
                                        MEQQAVVGVGNIYATESLYLSGIH
                                        PATPANEVSYAQIVILVAHIKTILQKAIKLGGST
                                        LRDFTVADGQTGYFQQTLNVYGRQ
                                        GNACPHCESTLENIKLNGRASVYCPLCQPIISM"
gene            complement(423686..4262 /gene="relA"
                26)
                                        /locus-tag="Psyc-0343"
CDS             complement(423686..4262 /gene="relA"
                26)
                                        /locus-tag="Psyc-0343"
                                        /EC-number="2.7.6.5"
                                        /function="RelA produces pppGpp
                                        (or ppGpp) from ATP and GTP (or
                                        GDP). SpoT degrades ppGpp, but may
                                        also act as a secondary ppGpp
                                        synthetase"
                                        /note="The two proteins are
                                        strongly similar. In many species,
                                        a single homolog to SpoT and RelA
                                        appears reponsible for both ppGpp
                                        synthesis and ppGpp degradation"
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                                        /db-xref="GI:71037904"
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                                        HINIDVPTWLDNVAKRIGQDSVPNLSAACAFIRK
                                        HMNTSASERSGAYVTGIGMTDILT
                                        YLYQDEDALVAAMLYRSARQSIISLNDIEKKFGA
                                        DISTLVKDTLAMGQLSEIIESNKR
                                        LEDHFVNNQRDQLSNIYSMLISVTNDVRVVLIKL
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                                        VMTIYAPLAHRLGIAQLKWELEDLAFRYLAPDRY
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                                     DELERIYIFSRDGDITELPKGATVLDFAYYVHTQ
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                                     DFAPTIDKRESGKLDAYKIQIDGLDNIEVGLAGC
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                                     /protein-id="AAZ18213.1"
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                                     RTSFEEGDAVNITANPNPERVVPPCPHFGVCGGC
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                                     QANVAPDHWLEPVVGDRLGYRTKARLGVRYVAKK
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                                     DPRIGFEIENLKTLISTLESRNKIAQLELAMGEY
                                     LPELPDGDQPVALIVRNLEPLSDA
                                     DIDKLKVFFAARNWQLYLQPKGADSIQRIALTAA
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                                     FSGLGNFSLPLARLVGETGSVVGV
                                     EGSEAMTIRAADNARRNGINNTEFYSQDLTHDCT
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gene            complement(428425..4292  /locus-tag="Psyc-0345"
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CDS             complement(428425..4292  /locus-tag="Psyc-0345"
                40)
                                     /codon-start=1
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                                     /db-xref="GI:71037906"
                                     /translation="MSQAFSSDPILVFDIETVAD
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                                     FSLTADKFSEEEILAKFFRAFNDI
                                     EKLPKLISWNGSGFDIPVLIYRAMQYDLAAPWLF
                                     EEGERIKNMRFDNYVNRFHTRHID
                                     LMDRFSQYGASRREAMDVVASLYGLPGKTDVDGS
                                     MVGELVSNNDWQTLSIYCESDVMN
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                                     TQADGTPRHQAFLNDWLNS"
gene            complement(429328..4302  /gene="cysM"
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CDS             complement(429328..4302 /gene="cysM"
                84)
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                                        /EC-number="2.5.1.47"
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                                        Selenoamino Acid Metabolism,
                                        Sulfur Metabolism: Fixation"
                                        /note="Cysteine Synthase B (CysM)
                                        can use thiosulfate to produce
                                        cysteine thiosulfonate in addition
                                        to use of hydrogen sulfide."
                                        /codon-start=1
                                        /transl-table=11
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                                        /translation="MSATAPLNVNFITQITDLAD
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                                        AARDMALQMQADGKGIVLDQFNNP
                                        DNKQAHYLTTGPELWAQTEGKITHFISSMGTTGT
                                        ITGVAQYLKEQNPAIQIIGLQPDE
                                        EAAIAGIRRWPAAYMPGIFDADLVDEIMDIDQRV
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                                        DDSIDNAN"
gene            430705..434112          /locus-tag="Psyc-0347"
CDS             430705..434112          /locus-tag="Psyc-0347"
                                        /function="two component signal
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                                        /product="putative signal
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                                        QDKLGRMRAEQHVQRIAIVNQNNEVLATVGYGTD
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                                        VITGLFTLLILLLSLNIYSKRWIA
                                        PIYELRLQLQRTHVDNLYQPIPVESNGELNLLQQ
                                        DLVRTLRRLYVSFQELKEHAEQTE
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                                        LANISHELRTPLNSIDGFINLLAR
                                        HGELNPEQDLYVQTIRKSSAHLLALVNDVLDFSK
                                        IEAGKLVLDRHEFDLYDTIYDVVD
                                        MLSPVSAEKGLRMAVLFYNDVPMRVNGDALRLKQ
                                        VLTNIVGNAIKFTDSGDVVVRVSL
                                        DDYQDNYLMISVQDSGKGISLSDQKMLFQSFSQG
                                        DPSITRQYGGTGLGLVISKQLTRL
                                        MGGDIGFYDNMQENISNQGATFWFRMPAHVDVLE
                                        AATGQTIELPVLAPLASATDEFNV
                                        LIWINHTASIQVLKASLHHLPITLTQANSLPGLL
                                        ESLKEHGNYWDWVIVDDDTQDDMM
                                        ALLKQIRLHYQGKLAVFGYQVAADQALLNRYHAN
                                        ILYEPLDKRQLYAMLDTQKRSVPT
                                        GIAEPRWKGVTVLAVDDHLPNLLVLDALLSELGI
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                                        SAKTEKQSLSKKTQISKAVTRDDVSKSAVSALHI
                                        EDTTTEEKGKAQHKNSIDLIFMDI
                                        QMPRMSGHEAARQIRKIEAADSHIPIIALTAHGL
                                        ADERDKLIASGINDYVGKPISQPQ
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                                     INDEKQALTQAWEAHNRSMLAQIAHRILGGSRYT
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gene            434240..435052       /locus-tag="Psyc-0348"
CDS             434240..435052       /locus-tag="Psyc-0348"
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                                     /product="putative enoyl-CoA
                                     hydratase/isomerase family
                                     protein"
                                     /protein-id="AAZ18217.1"
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                                     VWRDVPVPVIAVLEGYCVGAGLQLALACDIRISH
                                     PDCKLSIMEAKWGLVPDMGLTQSG
                                     FGVVRADILKELAMTARTVNAEEGKELGLVSHCS
                                     DTPLEQAQQLAAEFSERSPDAVLA
                                     SKRVINAMFEQSAMTLYIEKVWQLKMMFGRNRKL
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gene            435269..436528       /locus-tag="Psyc-0349"
CDS             435269..436528       /locus-tag="Psyc-0349"
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                                     /product="MFS multi-drug efflux
                                     pump, Bcr/CflA subfamily"
                                     /protein-id="AAZ18218.1"
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                                     IASIICATTNNEYVLFTGRTLQALGACVGAVVTR
                                     AAIRDRLTAKQTAKAFSIMILVMG
                                     LAPILAPSLGAVFLQFFSWHSIFWFLAAFGTLNL
                                     LLTKFFFFETLSEENRNVRPAKEI
                                     LSQYWELLKDPTFNYPAIGGGLLMGAMFVYISSA
                                     SELIMDTYGLSATHFGWLFGMNAA
                                     GFVALTQLNQWLTNRFRILSILRFGAMMQVISAG
                                     ALFTLGIVFGTDAWLPLVLACIFF
                                     CIAGLGLTQPNSSAIALAFQQRRAGMASALQGSL
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                                     IAMFSLMSLGCYLIWQIDRNLNLDNAD"
gene            436838..437632       /gene="rpsB"
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CDS             436838..437632       /gene="rpsB"
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                                     /codon-start=1
                                     /transl-table=11
                                     /product="SSU ribosomal protein
                                     S2P"
                                     /protein-id="AAZ18219.1"
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                                     /translation="MATKNPTKIEMRDLLQAGAH
                                     FGHQTRFWNPKMGPYIFGARNKIH
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                                     GGMLTNWKTLRQSINRLKELEKQAEDGTFAKLTK
                                     REALERTRDMEKLERSLGGIKDMG
                                     GLPDAIFVVDVDHEAIAIKEAKNLGIPVIGIVDT
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gene            437862..438746       /gene="tsf"
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CDS             437862..438746       /gene="tsf"
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                                     factor Ts (EF-Ts)"
                                     /protein-id="AAZ18220.1"
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                                     /translation="MSEVKVSAKMVKELRDRTGL
                                     GMMECKKALEESNGDVETAIDNLR
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                                     LENNVTDVAAIAELPYGNDQTVEEARVSLVQKIG
                                     ENIQIRRVEVLEGANIAAYRHGLR
                                     IGVVVSYEGGSAETGKNLAMHIAAFNPVAIDDED
                                     VAADLLAREKDIIEAKARESGKPD
                                     NIVEKMIEGGLRKYLEEVTLLRQSYVMDNEKKVG
                                     DVLKAEGVKVLGFKRLEVGEGIEK
                                     KQEDFAAEVAATQALANK"
gene            complement(438893..4397 /locus-tag="Psyc-0352"
                14)
                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     1.000) with cleavage site
                                     probability 0.462 at residue 32"
CDS             complement(438893..4397 /locus-tag="Psyc-0352"
                14)
                                     /function="Bacterial lytic
                                     transglycosylases degrade murein
                                     via cleavage of the beta-1,4-
                                     glycosidic bond between
                                     N-acetylmuramic acid and
                                     N-acetylglucosamine, with the
                                     concomitant formation of a
                                     1,6-anhydrobond in the muramic
                                     acid residue."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="possible lytic
                                     transglycosylase"
                                     /protein-id="AAZ18221.1"
                                     /db-xref="GI:71037913"
                                     /translation="MINIAPFMTRCLSPILLTAV
                                     ALSSLPIAAQAGNMYIYKDKGGQV
                                     LLTNVNPSGNFDKFTKKVKVTYYKDSSLYDSGSS
                                     NSSNDYGSSSASSSGTRNSYDSYI
                                     LASAQRHGVDPGLMKAMMHTESAFNPNARSPVGA
                                     QGLMQLMPATARRFKVSNPWNPAD
                                     NIEGSAKYIAWLMRRFNNNVEFAVAGYNAGEGNI
                                     DKYNGIPPFKETRNYVKSVMSRYH
                                     SLYKNDSGLSGNSMNANNSNIGTTSNGGGIQNVS
                                     YGTSSNSNSPSYANSAYLALR"
gene            complement(440145..4408 /locus-tag="Psyc-0353"
                34)
                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     0.621) with cleavage site
                                     probability 0.473 at residue 21"
CDS             complement(440145..4408 /locus-tag="Psyc-0353"
                34)
                                     /codon-start=1
                                     /transl-table=11
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                                     protein"
                                     /protein-id="AAZ18222.1"
                                     /db-xref="GI:71037914"
                                     /translation="MSFDNVFVATLAAILLTLTA
                                     HIIARILARKLSWLPMVITALVLV
                                     VILLFIFRWDYNHYYGVAKPVFDHLLGYVTVLLA
                                     IPLAAMNFKGLPVKKLVLIVAMAS
                                     LIGALLPMSLAYLFSLSHDTILAFASRSVTTPIG
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                                     LSIADLIKAPLAMANLIIIVSGII
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                                     WVPIFVTALSV"
gene            complement(440866..4412  /locus-tag="Psyc-0354"
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                                     2.0 HMM (Signal peptide probabilty
                                     0.854) with cleavage site
                                     probability 0.409 at residue 29"
CDS             complement(440866..4412  /locus-tag="Psyc-0354"
                94)
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gene            complement(441586..4430  /gene="hflX"
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                                     /transl-table=11
                                     /product="probable GTP - binding
                                     protein, possible phage lambda cII
                                     repressor"
                                     /protein-id="AAZ18224.1"
                                     /db-xref="GI:71037916"
                                     /translation="MEYFERHTGGERAIIVHLDI
                                     RQIQDPDDLGEFELLADSAGADRL
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                                     IVLFNHSLSPSQERNIEALVQCRV
                                     LDRTGLILDIFAQRARTYEGKLQVELAQLNHLST
                                     RLVRGWTHLERQKGGIGLRGPGET
                                     QLETDRRLLQVRVMQLKSRIEKVRQTRAQGRARR
                                     QKSDVPTISLVGYTNAGKSTLFNR
                                     LVDENIYAADKLFATLDPTLRRLDWQGVGRVVLV
                                     DTVGFVRHLPHELVESFHATLEET
                                     LEADLLLHVIDSSSEDMHEQIQAVKDVLAEIDND
                                     VPVLNVYNKIDLTDEPARIGYASE
                                     GQPNRVYVSSRENLGMEELSLAVQQLLTGTLTTF
                                     DLTLPYNAGQLKNALYELGVIQEE
                                     SYDDSGHECLTIRLPSDRLRQLLGQANLEPLDVL
                                     PLAQATLLMPILEEFEKPDEDEEQ
                                     TMTDAEEKAFAEFEALNAEAERAAQDLITEDIQT
                                     PDSQK"
gene            443633..444433           /gene="plsC"
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CDS             443633..444433           /gene="plsC"
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                                     /codon-start=1
                                     /transl-table=11
                                     /product="lyso-ornithine lipid
                                     acyltransferase"
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                                     /db-xref="GI:71037917"
                                     /translation="MSQPKSGFSIKQQLGRGKQI
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                                     SKAEIGEWPIFGKLAHAAGTVFIERGSGDVGSVA
                                     SQIANFLTKGFSVIFFPEATTTDG
                                     KKIKRIHGTLLQAAIDADVPVRPLVIAYVNKDGT
                                     LSEALPYYGKLTMKDSLKKVLDSK
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                                     DVTAYVLPLEAIDPKGLTKSQLTDLLQARMREGL
                                     AELHSRVLTKIAKV"
gene            complement(444568..4456 /locus-tag="Psyc-0357"
                08)
CDS             complement(444568..4456 /locus-tag="Psyc-0357"
                08)
                                     /codon-start=1
                                     /transl-table=11
                                     /product="putative oxidoreductase,
                                     aldo/keto reductase"
                                     /protein-id="AAZ18226.1"
                                     /db-xref="GI:71037918"
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                                     IQALNDEIKKGRIRAYGLSNDTAWGLMRYLWEAD
                                     KNGLIAPITVQNPYSLLNRLYEVA
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                                     GARLTMYDRFARYTNEQALAATAQ
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                                     EAVHTQQPNPSP"
gene            complement(445651..4461 /locus-tag="Psyc-0358"
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                                     NPEIGMLVEFEDKGKNTLPGTISAITNDEVEVDF
                                     NHPLAGQSVLFKIKIFQVTPPGVT GIKLI"
gene            446465..447346       /locus-tag="Psyc-0359"
CDS             446465..447346       /locus-tag="Psyc-0359"
                                     /function="Autonomous mobile
                                     genetic elements such as
                                     transposon or insertion sequences
                                     (IS) encode an enzyme,
                                     transposase, that is required for
                                     excising and inserting the mobile
                                     element."
                                     /note="There are 9 addittional
                                     ORFs identical to this one."
                                     /codon-start=1
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                                     /product="transposase, IS4 family"
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                                     CAAKQERYYGFEGHLLVNLSGMIK
                                     GFTFAPANVDERAVAPDITDNIYGLLGADKGYIS
                                     PSLTQYYDAQGVDLQTPLRANMKE
                                     DRPKPVVKRLMKARRIVETVIGQLSERFNIQRVR
                                     ARDLWHLSHRLIRKILSHNLCFVL
                                     NKKLGNPPLQFELLISS"
gene            448233..449150       /locus-tag="Psyc-0360"
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CDS             448233..449150          /locus-tag="Psyc-0360"
                                        /note="Contains TPR repeats, SEL1
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                                        /transl-table=11
                                        /product="conserved hypothetcial
                                        protein"
                                        /protein-id="AAZ18229.1"
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                                        QKAAEQGHIASQFNLGSLYRDGKGVQQDFSLAAE
                                        WYQKAAEQGHIASQFNLGSLYQDG
                                        KGIQQDFALAVKWYQKAAEQGHIASQFNLGSLYQ
                                        EGKDVQQDFALAAKWYQKAAEQGH
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gene            complement(449214..4494 /locus-tag="Psyc-0361"
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CDS             complement(449214..4494 /locus-tag="Psyc-0361"
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CDS             449893..450381          /locus-tag="Psyc-0362"
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                                        QEKWDSTCADLIHKVRHHLKEEENKFFKEAKKIL
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gene            complement(450659..4511 /gene="lspA"
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CDS             complement(450659..4511 /gene="lspA"
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                                        Aspartic peptidase. MEROPS family
                                        A08"
                                        /protein-id="AAZ18232.1"
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                                        DMLFLEKKREA"
gene            complement(451302..4541 /gene="ileS"
                27)
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CDS             complement(451302..4541 /gene="ileS"
                27)
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CDS         complement(454611..4551  /locus-tag="Psyc-0365"
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                                     DYPIVTVAIKSGSDQDLGGYLQEHNYNFTTINDQ
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gene        complement(455427..4570  /locus-tag="Psyc-0366"
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CDS         complement(455427..4570  /locus-tag="Psyc-0366"
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                                     activity:adenine deaminase that
                                     hydrolyses adenine to form
                                     hypoxanthine and ammonia which is
                                     important for adenine utilization
                                     as a purine and also as a nitrogen
                                     source"
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                                    IVVSMDKMNHIGQFYPADRMVEIEAGVVTQQLQQ
                                    FAESKDLYYPVDFASAGSSQIGGN
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                                    LGFVTHAQIKLERQPKDLNVMVLGMDSFNDVMNV
                                    LSAFQAKIDLTAFEFFDDVAIDKL
                                    MAHGQVQEPFESRTKFYTLLEFEAPYEPIMDKAM
                                    AIFEDCMEQGWVVDGVMSQNLAQA
                                    EELWKLREYISETISVFTPYKNDVSVLISYVPEF
                                    IAEIDHIVSSNYPDFEVCWFGHIG
                                    DGNLHLNILKPENMSKDNFFAECQVVNKHVFETV
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gene                460224..461450  /gene="serA"
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CDS                 460224..461450  /gene="serA"
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                                     ESGKILGAAIDVFPKEPKSADEEF
                                     ESPLRKFDNVILTPHIGGSTQEAQANIGLEVADK
                                     FVRYSDQGNTATAVNFPEVSIPFK
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CDS                  complement(461573..4626 /locus-tag="Psyc-0370"
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                                     AMFCTGGIRCEKSTAFMREQGFEE
                                     VYHLEGGILKYLEEVPASDSMWEGDCFVFDNRVS
                                     VNHNLEKGSYEQCFACRMPITQAE
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gene                 complement(462797..4638 /locus-tag="Psyc-0371"
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CDS                  complement(462797..4638 /locus-tag="Psyc-0371"
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                                     SFNYSSTIERLYSHSNINFIHGKA
                                     GKNSNKKIVLGISELQNQILIDNKAYGFVKYYQK
                                     LVNNTDYQFLRPKSPIVAIENKMK
                                     SPSLTKYHPIEVYIWGHSLDSSDSDYIHEIFSFN
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                                     VK"
gene            complement(464315..4648 /locus-tag="Psyc-0373"
                96)
                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     1.000) with cleavage site
                                     probability 0.993 at residue 22"
CDS             complement(464315..4648 /locus-tag="Psyc-0373"
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                                     VQPNLQQARGWLEKAAMRGDNRASYTLALLDEKQ
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gene            complement(465299..4659 /locus-tag="Psyc-0374"
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CDS             complement(465299..4659 /locus-tag="Psyc-0374"
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                                     AREAVITFPNFAHWQNRIHLGLKGIMPVSEALPY
                                     EWYNTPNIHLCTFKDFEKLCAQHD
                                     IHIINRFAVSDSEKGHSSLMTALIRRAPNLLADV
                                     AIYRVSKQKPE"
gene            complement(465913..4672 /gene="metX"
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CDS             complement(465913..4672 /gene="metX"
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                                     /EC-number="2.3.1.31"
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                                     Sulfur Fixation and Metabolism"
                                     /codon-start=1
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                                     /protein-id="AAZ18244.1"
                                     /db-xref="GI:71037936"
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                                     PYTDVVLEDWGKSGIRSVQILSPA
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CDS             complement(468847..4692 /locus-tag="Psyc-0377"
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                                     PVHHQNIDESRIDELLVEENLDDS
                                     HYPNIVDIADRDAAKLSNDNDF"
gene            complement(469527..4723 /gene="polA"
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                                     /locus-tag="Psyc-0378"
CDS             complement(469527..4723 /gene="polA"
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                                     /locus-tag="Psyc-0378"
                                     /EC-number="2.7.7.7"
                                     /function="DNA-directed DNA
                                     polymerases are the key enzymes
                                     catalyzing the accurate
                                     replication of DNA. They require
                                     either a small RNA molecule or a
                                     protein as a primer for the de
                                     novo synthesis of a DNA chain.
                                     This protein also contains 5'-3'
                                     exonuclease domains."
                                     /codon-start=1
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                                     /product="DNA polymerase I"
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                56)
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                                        /function="Involved in response to
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                                        SADEFQQLVEKANKVCPYSKAIHGNVDSEVTSEV
                                        K"
gene            474234..475829          /gene="prfC"
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CDS             474234..475829          /gene="prfC"
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                                        TPIISFVNKLDRQIREPLELLSEI
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                                     PRHRDRIAFLRVCSGKYEKGMKLK
                                     HVRLGKDVRIADALTFLAGDRAALEEAYPGDIIG
                                     LHNHGTISIGDSFTEGEELNFTGI
                                     PHFAPELFRRVILKDPLKSKALQKGLQQLSEEGA
                                     TQVFMPQINNDLILGAVGVLQFEV
                                     VAHRLKEEYKVQCIFEPVSIATVRWIHCDDEVAL
                                     AKFKRKAHDQLSLDGGGHLTYLAP
                                     SRVNLQLMQDRYPEVTFSNTREH"
gene            476550..476816       /locus-tag="Psyc-0381"
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CDS             476550..476816       /locus-tag="Psyc-0381"
                                     /note="conserved hypothetical
                                     protein"
                                     /pseudo
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CDS             476897..477853       /locus-tag="Psyc-0382"
                                     /note="Forkhead-associated (FHA)
                                     domain.  The domain is present in
                                     a diverse range of proteins, such
                                     as kinases, phosphatases,
                                     kinesins, transcription factors,
                                     RNA-binding proteins and metabolic
                                     enzymes which partake in many
                                     different cellular processes"
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                                     LTEALGDLTLTVTDSLSIGRGSDN
                                     DLVLGSKQISRNHAQLSVLNGQLYVKDLESSNGT
                                     FINDERIAANESKYLEANDTLGFA
                                     SLSFQVSAPVAATAIPEQAVADKPTLMLSPDTEI
                                     ALIVEAEPVVKETGISEILLAADS
                                     AEPVLSEVEYSPTETMPIPSAHQESLVEQPVLAD
                                     EPVINKATVSETFSETSYASEAPV
                                     IEAAVELEHDKTTKTALQEEADPDVLRAKQAATS
                                     QFSGTANLGQSRDLGTTGNNAMDQ
                                     ALDNPANEGAVEKKPSGGWFIWVFVAIIIIGLAL
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gene            478244..478319       /locus-tag="Psyc-R0012"
tRNA            478244..478319       /locus-tag="Psyc-R0012"
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gene            478385..478468       /locus-tag="Psyc-R0013"
tRNA            478385..478468       /locus-tag="Psyc-R0013"
                                     /product="tRNA-Tyr"
gene            478555..478628       /locus-tag="Psyc-R0014"
tRNA            478555..478628       /locus-tag="Psyc-R0014"
                                     /product="tRNA-Gly"
gene            478733..478807       /locus-tag="Psyc-R0015"
tRNA            478733..478807       /locus-tag="Psyc-R0015"
                                     /product="tRNA-Thr"
gene            479294..480484       /gene="tufBa"
                                     /locus-tag="Psyc-0383"
CDS             479294..480484       /gene="tufBa"
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                                     /EC-number="3.6.5.3"
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                                     /product="elongation factor Tu
                                     (EF-Tu)"
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                                     /db-xref="GI:71037943"
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                                     KDYASIDSAPEEKARGITINTSHVEYDTPSRHYA
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                                     ILVVSATDGPMPQTREHILLSRQVGVPYIVVFMN
                                     KCDVVDDEELLELVEMEVRELLSD
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                                     LNVLDTYIPEPERDIDKAFLMPIE
                                     DVFSISGRGTVVTGRVESGIVRVGEEIEIVGIRD
                                     TQKTTCTGVEMFRKLLDEGRAGEN
                                     CGVLLRGTKREDVQRGQVLAKPGSITPHTKFDAE
                                     VYVLSKEEGGRHTPFLNGYRPQFY
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gene                 complement(480663..4812 /locus-tag="Psyc-0384"
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CDS                  complement(480663..4812 /locus-tag="Psyc-0384"
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                                     ICSNDLDNIHQAINQINTHDNHSKFTMIVFNERE
                                     IRWDTPDIPIIDSLLLNYFTLSQK
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gene                 481437..481907          /gene="rimI"
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CDS                  481437..481907          /gene="rimI"
                                     /locus-tag="Psyc-0385"
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                                     /product="possible
                                     ribosomal-protein-alanine
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                                     /protein-id="AAZ18253.1"
                                     /db-xref="GI:71037945"
                                     /translation="MLAIKVLSTASVENHPIIQA
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                                     QDIIDLLAVYQSKKVVGYCLYQVVFEQAEILRIG
                                     THPDYQRQGVASRIFARLEAELQA
                                     KQVESLLLEVRADNVPAIALYEQQAFAVIHKRKG
                                     YYHLLGQPAVDALIMQRVYN"
gene                 complement(481988..4824 /locus-tag="Psyc-0386"
                     22)
CDS                  complement(481988..4824 /locus-tag="Psyc-0386"
                     22)
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                                     /product="putative transcriptional
                                     regulatory protein, MerR family"
                                     /protein-id="AAZ18254.1"
                                     /db-xref="GI:71037946"
                                     /translation="MASDTSFLLIGKLATKANTT
                                     KDTIRHYDQLGLLKSRKRQAGSRL
                                     YTEFHSECVERIELIKSAQAIGFTLTEIKDSLND
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                                     QQATISLMIEMLTERIDILEHMKADSDYELDINM
                                     CKKILPSS"
gene                 complement(482733..4835 /locus-tag="Psyc-0387"
                     39)
CDS                  complement(482733..4835 /locus-tag="Psyc-0387"
                     39)
                                     /function="Controls protein
                                     half-life through N-end rule
                                     degradation pathway."
                                     /codon-start=1
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                                     /product="probable
                                     leucyl/phenylalanyl-tRNA--protein
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                                        transferase"
                                        /protein-id="AAZ18255.1"
                                        /db-xref="GI:71037947"
                                        /translation="MNNINDSSAIHITPETFVKQ
                                        IRSLGRYNFPEPALVDPDGIGIVG
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                                        PRCVMQPTDYQPSKSLRKQANNAR
                                        WQLTLNQAFNEVIHACSLPRSNGLPEGEHTWIHD
                                        DMIEAYNELHAQGFAHSVEVWDDQ
                                        GQLVGGLYGLKIGSIYFGESMFHIASNASKLAFW
                                        GLMRLCTQSNVTLVDCQLPNEHLM
                                        SLGAITLSRTEFLTQLDTLISNGSDAWHKNSHRP
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gene            complement(483610..4846 /gene="trxB"
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                                        /locus-tag="Psyc-0388"
CDS             complement(483610..4846 /gene="trxB"
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                                        /product="putative thioredoxin
                                        reductase"
                                        /protein-id="AAZ18256.1"
                                        /db-xref="GI:71037948"
                                        /translation="MATDNTAPRHEKLIILGSGP
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                                        RFGTELVYDHINAVNLNVRPFELT
                                        GNNGSYTCDALIISTGASAQYLGLESETKFRGLG
                                        VSACATCDGFFYKDKKVAVIGGGN
                                        TAVEEALYLSNIASEVTLVHRRDSLRSEKILQDK
                                        LFEKAKNGNVKIEWNHSVKEVVGD
                                        DMGVNGVVIESMLDGSTKQLDVFGMFVAIGHKPN
                                        TDLFKGQLEMKDGYLIVNSGLNGN
                                        ATQTSIEGVFAAGDVADHVYRQAITSAGTGCMAA
                                        LDAEKYLDAIGEAVAKDHTYASTL TADKEA"
gene            485598..488804          /gene="ftsK"
                                        /locus-tag="Psyc-0389"
CDS             485598..488804          /gene="ftsK"
                                        /locus-tag="Psyc-0389"
                                        /function="A mutation in FtsK
                                        causes a temperature sensitive
                                        block in cell division and it is
                                        involved in peptidoglycan
                                        synthesis or modification."
                                        /codon-start=1
                                        /transl-table=11
                                        /product="DNA translocase FtsK"
                                        /protein-id="AAZ18257.1"
                                        /db-xref="GI:71037949"
                                        /translation="MTYTGNDPSWSHISSDMTAI
                                        NNMGGEMGAWLSDLLYSFFGFGAW
                                        WLLAFLVYESVLIWWDNKPTFWLLRLVAYVFLIL
                                        SSSALFAQLIALAQQVADPISSGL
                                        KGVAGGIIGLELQARLAQLLSQWGSVTFLAVFVI
                                        ITATFAFNIHWLSIYEKIKTLSWF
                                        GSGVKNLDRTLDANQIANISNVAKHSADDTTINE
                                        NAAPEYEQLPLELQAAGHANTKEK
                                        DGKSGRFNTALTDFLSSSGLSASVKASMAATVQI
                                        ASEMSRREEQLQTAATTTGNSASN
                                        LNKKSAPVTNAMPTPIRKVEPSFAWNDANTVDDL
                                        LANQIANEQDTIPYDAVDVPYLDV
                                        SASESFDSSNIETSSASPVFDITQEDTQQPTQQQ
                                        AMHSLDDFAATLSIDQTDQTDISE
                                        SAPSVDSLVDAWLVEHAAVPETTDFNHEQELSVV
                                        ETLVETAAAPTKQQNAISLNDAAD
                                        ELSNNSSAELPENLESSCNADVTNALGITDMTPT
                                        NTPPANPKASPMAESTATISSIES
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                                        ADDIDALVMPHISDDIAFSQKSRS
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                                     MQTAAYRSSLSPIPELSILDKPDPNRQPSYTLAE
                                     LEQLSELLEIKLQEFNVKANVVNA
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                                     REMVRLIELLDTEKFKDPKAQISMAMGKDIGGKP
                                     IITDLARAPHMLVAGTTGSGKSVL
                                     VNAMLLSMLLKYTPNELRMILIDPKQLELANYND
                                     IPHLLTPVVTDMTEAASALSWCVA
                                     EMERRYQLMSLLKVRKLNEFNKKVIAAEKAGNPM
                                     LDPLWRPNDSVSISQAPKLKTLPM
                                     IIIVADEFADMIMQVGKQAEELITRLAQKSRAAG
                                     IHLILATQRPSVDVITGLIKANIP
                                     VRAALRVNSKVDSRTILDSGGAEDMLGNGDMLFL
                                     GPGQIEPDRVHGAYVSDEEVNSVC
                                     DAWRERGAPDYIDNMAGNFELSSPSGGSSAANAS
                                     GEDDDLYNEAVGFIMETRKVSASS
                                     IQRKFSIGYNRAARIVDSMEEAGLVSSMGKSGKR
                                     ELLM"
gene            complement(489143..4896 /locus-tag="Psyc-0390"
                31)
CDS             complement(489143..4896 /locus-tag="Psyc-0390"
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                                     KNPSDANLAQYREQEGQAILAAHAAAGREQLWVL
                                     DVKGKMLSTENLADKLADGMQQGD
                                     DIALVIGGADGVSPEVLAKADVKWSLSALTLPHP
                                     LVRVVLMEQLYRAMSINHNHPYHR GN"
gene            complement(489872..4904 /gene="dnaQ"
                83)
                                     /locus-tag="Psyc-0391"
CDS             complement(489872..4904 /gene="dnaQ"
                83)
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                                     /EC-number="2.7.7.7"
                                     /function="The epsilon subunit
                                     contains the proofreading 3' -> 5'
                                     exonuclease activity of DNA
                                     polymerase III core enzyme
                                     (responsible for chromosome
                                     replication)."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="probable DNA polymerase
                                     III, epsilon subunit"
                                     /protein-id="AAZ18259.1"
                                     /db-xref="GI:71037951"
                                     /translation="MRMNWLKKLSVAWQKNQLQR
                                     PELASMFAMPAPEQWVAIDCEMTG
                                     LNPKKHHLLSVAAIHINGDKIDTGNGLHLLCRPP
                                     VMPKSDTIVIHGLRTADVEHAMSY
                                     DEMLSLLLPFIGNRPLVGFFPQIDVGFLNPLVKR
                                     YMGTHLPNEVIDIRSLYSRRMMGR
                                     SQGLPSQAQHLNSILKHYNIPELGTHDAYNDAIM
                                     TAMAFLHVR"
gene            complement(490541..4924 /locus-tag="Psyc-0392"
                99)
CDS             complement(490541..4924 /locus-tag="Psyc-0392"
                99)
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                                     /db-xref="GI:71037952"
                                     /translation="MPHLDFTQPPFDVLSAAERQ
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                                     TDINELIMPYQFRAVEDTLLLQVNGTAIDKISAQ
                                     NYLVRQLVSENLPERLKALQLRRS
                                     GQHLDAASYDDQQEVQQIMLQPVIDITLLPVHIV
                                     GADDNLYQAARTMTEAGLKHVLVR
                                     PTGYLQDKDSFDRTLGILTDNDICRAVSDQKNPA
                                     TTPCQGYASFHLRTIDADDDIGDA
                                     LLTMTRYRIHRLPVIDANGKVIGVLGQSDMLAHI
                                     GHHSQLISIQIEQATDLPSLATAV
                                     ELIGRYIRAQYQNGIKMGNVSRMVQTLNAQVFTK
                                     LWQLIVPDEVMENTCVIVMGSEGR
                                     GEQIMRTDQDNALIIRDGFTHPELARFAETFNQH
                                     LANLGYPLCEGNIMMTNPMWRQPL
                                     KPFKAQISAWYKNTDPIHSIYLSAIFDGEYVCGD
                                     ESLLIQIREHLKTAHRQSDLMFVR
                                     QFARAALQFGDINQWWQKLVPLLGGKPISYTIDL
                                     KKAGIFPLVHGIRTLALENDIFTD
                                     PSSKGRLKALVQARALTQERADTLLEALEFFMAQ
                                     RLSVALSTDNKHAQEVDPRTLSAL
                                     ERDLLKECLAVVKSFKGQLSRQYQLEIG"
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CDS             complement(492825..4940 /locus-tag="Psyc-0393"
                51)
                                     /EC-number="2.6.1.11"
                                     /function="Aminotransferase,
                                     Lysine biosynthesis?"
                                     /note="Class not determined"
                                     /codon-start=1
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                                     /product="succinyldiaminopimelate
                                     aminotransferase"
                                     /protein-id="AAZ18261.1"
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                                     /translation="MNHNLTTLHPYPFAKMATLL
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                                     EKRFFLNHVNPNTQVLPVMGTREA
                                     IFSIVQAVINHQTETISQTATLNQSPVVVMPNPF
                                     YQIYEGAAILAQATPYFIPCTADN
                                     GFKGDFRSVPKDVWMRTQLLFVCSPNNPTGSVMT
                                     MDDWEQLLRLSDQYGFIIASDECY
                                     SELYFDKAPIGLLQACAALGRHDFKNCLVFHSLS
                                     KRSNLPGLRSGFVAGDATILDSYL
                                     QYRTYQGCAMPIPHQLASIAAWEDEKHVAHNRAL
                                     YQEKFALWMSELGALLDLRMPEAG
                                     FYFWIKAPEQFDGDDELFVKALYEHANIHALAGR
                                     YLSREVNGKNPGQGYVRIALVASV
                                     EESREAIRRIRQLLGA"
gene            494365..495033       /locus-tag="Psyc-0394"
CDS             494365..495033       /locus-tag="Psyc-0394"
                                     /note="Two transmembrane helices
                                     predicted."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="hypothetical protein"
                                     /protein-id="AAZ18262.1"
                                     /db-xref="GI:71037954"
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                                     QLTLLRERQMFWFGDNSFMMWLLWQLVSYIVVAM
                                     VLMLLSKLLDISFPLWQYIALFVV
                                     QTLIFVVMLGFKDRFARQLEYKINQADLSREEML
                                     NEMTILASDSLYRDVHAKAPITLK
                                     QIYRYYNAEFRLVSLQRLLQKEVDAGRLMYGDQK
                                     IEAALLPLELADDALKEYARGIIY KSLI"
gene            complement(495044..4977 /gene="glnD"
                91)
                                     /locus-tag="Psyc-0395"
CDS             complement(495044..4977 /gene="glnD"
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                91)
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                                        /function="Signal transduction:
                                        Inactivates protein PII ->
                                        upregulation of glutamine
                                        synthesis genes"
                                        /note="Senses intracellular
                                        glutamine levels via ACT domain"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="probable protein-P-II
                                        uridylyltransferase"
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                                        NMTTAPLSLSTDTSLIEKSLFGIP
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                                        LIGLFKWFELDKTDLALFATGGYG
                                        RGELSLHSDIDILLLMPHEIDADTSSKIDNLVAL
                                        LWDIGLEPALSVRSVSECLEAALD
                                        HTIASALLEARLLIGNETLQDVPHQIVNNQWSPR
                                        AFYDVKIDEAKARYLQHNATEYNL
                                        EPNIKTAPGGLRDIHIVGWVTKRYFRVSKLYDLV
                                        QQNFLTEKEFDELSFSEGYLWQIR
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                                        QPNAAVERFMRDYYRCAMQISTLS
                                        EMLTNHYYETIIEPQLPDEERPKKQPINARFNQV
                                        GEQIAMAHHRVFAQHPESILEMFL
                                        LMGQYGIKNVRTHTLRALKIAARGIDQAYRDNPT
                                        HQTLFLANLKEQNYLFHRLRTMNR
                                        YGVLGNYIPAFAQVTGLMQYDLFHRYTVDAHTLF
                                        LIRILHRFIDPHFYEDFPLVSSIF
                                        QRIERKEILVLAAMFHDIAKGRGGNHSQLGEIES
                                        IEFCLAHGMSNADANLVGWLTRYH
                                        LLMSMTAQKKDISDPEVVTLFADLVGNVTHLNHL
                                        YVLTVADMNATNPQLWNSWRATLM
                                        KQLYSQTRRILRADIDAPTNRQDMISATRKQALM
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                                        EYFLREIAEDILWHTEAILNHPPIGRASNADSPP
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                                        VNLFAVTMAVFDQMNLDVLDARIITATRDFALDS
                                        YVLLDRSGTLLVDSDSQQELKQRL
                                        IDAFKNPTAPKLTHKRIPRQLKHFDVETTINFEF
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                                        QVFLQQQIEVHAARITTLGERAEDMFYISDQNDQ
                                        ALSANKLKTLKTALIESLSVHNDS I"
gene            complement(497967..4987 /gene="map"
                61)
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CDS             complement(497967..4987 /gene="map"
                61)
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                                        /EC-number="3.4.11.18"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="methionine
                                        aminopeptidase, type I"
                                        /protein-id="AAZ18264.1"
                                        /db-xref="GI:71037956"
                                        /translation="MMTKKSLIQSPEAIEKMRVA
                                        GKLASDVLVMLDEHVRVGISTEAL
                                        NQIAHDYIVNVQQAIPAPLNYNGFPKSICTSINH
                                        VVCHGIPTENKLLKDGDIINIDVT
                                        VIKDGYYGDTSKMWIVGNGSIMAQRICKVAQDAL
                                        YAGMSVVKNGARLGDVGAAIQAVV
                                        EPERFSIVREFCGHGISNEFHHEPQVMHYGKKGT
                                        GFELKTGMTFTIEPMINEGKWQTK
                                        ILPDEWTAITKDRKLSAQWEHTMVVTIDNGCEVFT
                                        TRPEEDLSFLTQ"
gene            499186..499533          /locus-tag="Psyc-0397"
CDS             499186..499533          /locus-tag="Psyc-0397"
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                                     /note="Signal peptide predicted.;
                                     Signal predicted by SignalP 2.0
                                     HMM (Signal peptide probabilty
                                     0.716) with cleavage site
                                     probability 0.275 at residue 40"
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                                     GTAKVSTLYRIRPDGSERQLIDQL
                                     NGYIYAPAWSADV"
gene                 499505..500203  /locus-tag="Psyc-0398"
                                     /pseudo
CDS                  499505..500203  /locus-tag="Psyc-0398"
                                     /note="possible tolB protein"
                                     /pseudo
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CDS                  500233..500403  /locus-tag="Psyc-0399"
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                                     KYEGLDHQKEDK"
gene                 500449..500598  /locus-tag="Psyc-0400"
CDS                  500449..500598  /locus-tag="Psyc-0400"
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                                     /transl-table=11
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                                     /protein-id="AAZ18267.1"
                                     /db-xref="GI:71037959"
                                     /translation="MAHKKVNLPQKICPVCQRPF
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gene                 complement(500671..5022 /gene="dcm"
                     33)
                                     /locus-tag="Psyc-0401"
                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     0.839) with cleavage site
                                     probability 0.547 at residue 22"
CDS                  complement(500671..5022 /gene="dcm"
                     33)
                                     /locus-tag="Psyc-0401"
                                     /function="C-5 cytosine-specific
                                     DNA methylases specifically
                                     methylate the C-5 carbon of
                                     cytosines in DNA to produce
                                     C5-methylcytosine. In bacteria,
                                     these enzymes are a component of
                                     restriction-modification systems."
                                     /note="Citation: Lauster R,
                                     Trautner TA, Noyer-Weidner M.
                                     1989. Cytosine-specific type II
                                     DNA methyltransferases. A
                                     conserved enzyme core with
                                     variable target-recognizing
                                     domains. J Mol Biol.
                                     206(2):305-12."
                                     /codon-start=1
                                     /transl-table=11
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                                     HKLIIGSIKELNQVLKSSPSMLKSINDADVVSGG
                                     PPCQSFSMAGLRELSNDRNTLPWE
                                     FMQFVKLTHPKIAVLENVSGILRAFRSEGKPYYA
                                     WFEIAKGFAALGYVPICLHVNARF
                                     AGIAQNRNRFILIAIRFDTLSQQLHSFNDIELSL
                                     IKPYFSFYQNIESSKTVKFDDIKV
                                     IDLTKGTDTNLVNTFLAPFFEYKENNFTVKDVID
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                                     LESSERKEVFDFLKGRSEILSEKA
                                     VNKLLEFDFLLLDGSFGKLSNEKEITMFFRQHLT
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CDS                  502506..503840  /locus-tag="Psyc-0402"
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                                     TKNATDGKVTITTSEAQEKTLNQQNKELLAEYGI
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                                     HFLVEEGFHNYEDQKQGESYKVLKPCQLITSEKI
                                     LNKKVSLYRPVTKKGDPRIWVYGL
                                     SSHVRADDELTFFIVDDLLYVLNLNSVDISDYKD
                                     LLFELKQSLDETAIELRDKLIEIA
                                     KQPLKSIMKGDTAIGMTIEHALGLTANSSKKPDY
                                     KGIELKSGRITKSKTRSNLFAQVP
                                     AWDKSVLKSSREIVDSYGYPDKDNGDQRLYCTVN
                                     VSNFNNQGLRLVVDLENDKVYEEH
                                     EIDGLIVVWEGQKLRERLLEKHHETFWISANVNI
                                     INGLEFYSLNGFTHTKNPMEHQLL
                                     PLIKQGVITLDHLIKRKNETGRTSEKGPFFKIKP
                                     QDLEMLFPEPVFYSLVKD"
gene                 complement(503979..5077
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                                     /locus-tag="Psyc-0403"
CDS                  complement(503979..5077
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                                     /locus-tag="Psyc-0403"
                                     /EC-number="2.1.1.13"
                                     /function="Methionine biosynthesis
                                     and metabolism"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="methionine synthase
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                                     /protein-id="AAZ18270.1"
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                                     PHMIKEIHLAHLESGADIIETNSFNGTRLSMADY
                                     DMQYLVPELNKTAAKIAREAADEY
                                     TAKNPDKPRFVAGVIGPTSRTCSLSPDVNDPAFR
                                     NITFDELVLNYREATLALMEGGVD
                                     IILIETIFDTLNAKAAIFAVTGVFDDIGFELPIM
                                     ISGTITDASGRTLSGQTAEAFYNS
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                                     VSAHPNAGLPNEFGEYDETADETA
                                     ALLEGFAKAGILNIVGGCCGTTPEHIRQIANMVA
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                                     KYPPRVIPEIAPACRLSGLEPFTI
                                     NSDSLFVNVGERTNVTGSKKFLRLIKTEAYTEAL
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                                     SGGVSNVSFSFRGNPIREAINSVF
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                                     PLMDGMNIVGDLFGAGKMFLPQVVKSARVMKQSV
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                                     VKGDVHDIGKNIVGVVLGCNGYDIVDLGVMVPCE
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                                     KPNFSLADFISPSDMHTDYLGGFTVSIVGTEALA
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                                     AFAEHLHELIRKEYWGYQPTESLTNEDMIKEKYV
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gene            508533..509117       /locus-tag="Psyc-0404"
CDS             508533..509117       /locus-tag="Psyc-0404"
                                     /note="fasciclin domain; Signal
                                     predicted by SignalP 2.0 HMM
                                     (Signal peptide probabilty 0.995)
                                     with cleavage site probability
                                     0.457 at residue 22"
                                     /codon-start=1
                                     /transl-table=11
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                                     /db-xref="GI:71037963"
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                                     LAGVLSNPNANYTILAPTNAAFMQ
                                     ALQETGMSKAQLFANKPLLTKILSYHVINAAAPI
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                                     "
gene            509429..510031       /locus-tag="Psyc-0405"
CDS             509429..510031       /locus-tag="Psyc-0405"
                                     /note="fasciclin domain; Signal
                                     predicted by SignalP 2.0 HMM
                                     (Signal peptide probabilty 1.000)
                                     with cleavage site probability
                                     0.656 at residue 21"
                                     /codon-start=1
                                     /transl-table=11
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                                     VPMVVKAADIPYGTAIETANGQTI
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                                     TVLLPK"
gene            complement(510427..5117 /locus-tag="Psyc-0406"
                61)
                                     /pseudo
CDS             complement(510427..5117 /locus-tag="Psyc-0406"
                61)
                                     /note="sodium/alanine symporter"
                                     /pseudo
                                     /codon-start=1
                                     /transl-table=11
gene            511927..512808       /locus-tag="Psyc-0407"
CDS             511927..512808       /locus-tag="Psyc-0407"
                                     /function="Autonomous mobile
                                     genetic elements such as
                                     transposon or insertion sequences
                                     (IS) encode an enzyme,
                                     transposase, that is required for
                                     excising and inserting the mobile
                                     element."
                                     /note="There are 9 addittional
                                     ORFs identical to this one."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="transposase, IS4 family"
                                     /protein-id="AAZ18273.1"
                                     /db-xref="GI:71037965"
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                                     RDNIHFMDGFPIPVCHYGRAYRHKNYQDLAAFSY
                                     CAAKQERYYGFEGHLLVNLSGMIK
                                     GFTFAPANVDERAVAPDITDNIYGLLGADKGYIS
                                     PSLTQYYDAQGVDLQTPLRANMKE
                                     DRPKPVVKRLMKARRIVETVIGQLSERFNIQRVR
                                     ARDLWHLSHRLIRKILSHNLCFVL
                                     NKKLGNPPLQFELLISS"
gene            complement(512800..5129 /locus-tag="Psyc-0408"
                64)
                                     /pseudo
CDS             complement(512800..5129 /locus-tag="Psyc-0408"
                64)
                                     /note="sodium/alanine symporter"
                                     /pseudo
                                     /codon-start=1
                                     /transl-table=11
gene            513935..514567       /locus-tag="Psyc-0409"
CDS             513935..514567       /locus-tag="Psyc-0409"
                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     0.996) with cleavage site
                                     probability 0.858 at residue 34"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="LemA family protein"
                                     /protein-id="AAZ18274.1"
                                     /db-xref="GI:71037966"
                                     /translation="MTRKSIVKPILLSAVLATST
                                     VGLTGCGYNNLQAQDEQVTASWSE
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                                     EARSRAGGITVTPEVLNDPKAMER
                                     YAAAQEQMTGALSRLMAVSERYPELKSDALFQDL
                                     QAQLEGTENRIAVARNRYIQEVQG
                                     YNTTVRQFPTNITAKVFGMSAKPNFSVANEKEIS
                                     TAPSVDFDNGGSKAAQ"
gene            514839..515999       /locus-tag="Psyc-0410"
CDS             514839..515999       /locus-tag="Psyc-0410"
                                     /note="Signal predicted by SignalP
                                     2.0 HMM (Signal peptide probabilty
                                     1.000) with cleavage site
                                     probability 1.000 at residue 26"
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                                     protein"
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                                     TANSVDADKLILNNPVIDQANILNPQEKQRLEAQ
                                     LRTIYQQGLAQAAVVIVPTTNGMP
                                     IFDYALQVAEKWQLGDKDIDDGLLLVVAVNDRDM
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                                     ITPLFKQNDYGAGILAGVTALQSRLSADPEVLAR
                                     ADAQAAERTAQQGSDELPSPIFLF
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                                     GGGLFMTIIMAIFLWLFLIARGGG
                                     SGKGGSGGGRGGRGGMIFLPGMGGGSGGGGFGSG
                                     GFGGGGGGFGGGGAGGSW"
gene            516094..516618       /locus-tag="Psyc-0411"
CDS             516094..516618       /locus-tag="Psyc-0411"
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                                     /transl-table=11
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                                     /db-xref="GI:71037968"
                                     /translation="MAENNASKSSFARWWRQVLF
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                                     SEYRVWDTEENTGVLIYVNVCEHK
                                     LEIVADRGISAHVSPTVWRAMCDKAVVGIANQKT
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                                     PSGNELSDTVVFLK"
gene            516806..517165       /locus-tag="Psyc-0412"
CDS             516806..517165       /locus-tag="Psyc-0412"
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                                     /product="hypothetical protein"
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                                     /db-xref="GI:71037969"
                                     /translation="MIDGIWWLVILIAVVIGLWL
                                     FAKSRSPNNLHDIKSKDKKKPIND
                                     ALQKTAKMIKQYFPDYGVTRKGSHLLINRQNTKI
                                     AMITIDPKLAASQRRLGDIPVFNY
                                     HRVPSRTQLDANLQEAE"
gene            517547..517894       /locus-tag="Psyc-0413"
                                     /pseudo
CDS             517547..517894       /locus-tag="Psyc-0413"
                                     /note="type I
                                     restriction-modification system, M
                                     subunit"
                                     /pseudo
                                     /codon-start=1
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gene            517955..518836       /locus-tag="Psyc-0414"
CDS             517955..518836       /locus-tag="Psyc-0414"
                                     /function="Autonomous mobile
                                     genetic elements such as
                                     transposon or insertion sequences
                                     (IS) encode an enzyme,
                                     transposase, that is required for
                                     excising and inserting the mobile
                                     element."
                                     /note="There are 9 addittional
                                     ORFs identical to this one."
                                     /codon-start=1
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                                     /product="transposase, IS4 family"
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                                     /db-xref="GI:71037970"
                                     /translation="MPIDEFIINIYLMVEQYYKI
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                                     RDNIHFMDGFPIPVCHYGRAYRHKNYQDLAAFSY
                                     CAAKQERYYGFEGHLLVNLSGMIK
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CDS             518942..520957       /locus-tag="Psyc-0415"
                                     /note="probable type I
                                     restriction-modification system,
                                     subunit M  (DNA methylase)"
                                     /pseudo
                                     /codon-start=1
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gene            520957..522330       /locus-tag="Psyc-0416"
CDS             520957..522330       /locus-tag="Psyc-0416"
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                                     subunit"
                                     /protein-id="AAZ18279.1"
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                                     ADTSEDIEGSGNFTQLVSDDLIFAGYHTVIARPF
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                                     VKGVKVFSITQSILKGVRIWLPSLDERETIANFL
                                     DFETAQIDTLIDKQKTLIQLLKEK
                                     RQAVISHAVTKGLNPDAPLKDSGVEWLGEVPEHW
                                     GVSKLKYLISEPLQYGANEAAEDV
                                     DKTQPRFVRITDVLPNGNLKDDTFRSLPQEIAEP
                                     YMLMDGDVLLARSGGTVGKSFIYR
                                     DSWGKCCFAGYLIKAKIDEEITPAEWFYLNTLTD
                                     FYWKWIESIQIQATIQNVSADKYN
                                     SFVIAVPPLEESYKIISYINYNLEVFDTLVMKAE
                                     QAIQLMQERRTALISAAVTGKIDV RGWVAPE"
gene            complement(522539..5228 /locus-tag="Psyc-0417"
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CDS             complement(522539..5228 /locus-tag="Psyc-0417"
                29)
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                                     /protein-id="AAZ18280.1"
                                     /db-xref="GI:71037972"
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                                     LSFYWEFMFARSLFQVADMEAQGP
                                     LLNRVSNLINQGHIQTTVGNNIGVISAANLRVVG
                                     NIGHVKSVYINTNFDCFL"
gene            523115..523795       /gene="gst"
                                     /locus-tag="Psyc-0418"
CDS             523115..523795       /gene="gst"
                                     /locus-tag="Psyc-0418"
                                     /function="Glutathione metabolism,
                                     Conjugates Glutathione with a
                                     variety of hydrocarbons."
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                                     /protein-id="AAZ18281.1"
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                                     /translation="MLKFYFHQTPNPLKVAAFLE
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                                        FSGQSVHFRHKAPEKIPYAINRYLREAERHYEVL
                                        DTHMEGREYIVGDEYSIADISAWG
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gene            524327..525019          /locus-tag="Psyc-0419"
CDS             524327..525019          /locus-tag="Psyc-0419"
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                                        DTSNVKFEKMAEPNLTFGENSVDVILATMVCHHM
                                        SNEEIIEFFKQALHTTKDKVIIND
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CDS             524974..526065          /locus-tag="Psyc-0420"
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                                        VELKLAARARRLGGRIRENTYLEYTTPATERTPF
                                        YFKLSTGEIIEAKSAFFATGKLSN
                                        NKDNKKIALPYFGFKLHFSHTENDHSLKMFSLDK
                                        AYLGIVPITETISNCACLAKREAV
                                        DAATSPEEHFRHLTQSHPVLKKIFTPLDLSAIDI
                                        LSGRAPAFTQKKPPNWPNSYWIGD
                                        TLASLYPAIGSGFAHSVDSAIQAVQSYLKQQPKL
                                        YRINYSKSIKTKVLLGNVFNAALL
                                        QPKVGQLALPLLKRSPKLVNLVLKKLDYV"
gene            complement(526062..5271 /locus-tag="Psyc-0421"
                50)
CDS             complement(526062..5271 /locus-tag="Psyc-0421"
                50)
                                        /EC-number="2.3.1.74"
                                        /function="acyltransferase
                                        activity"
                                        /note="Part of the pathway of
                                        flavonoids, stilbene and lignin
                                        biosynthesis."
                                        /codon-start=1
                                        /transl-table=11
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                                        /protein-id="AAZ18284.1"
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                                        RMALYKEHALPLAVSAIKQCMEQS
                                        DATFADITHVITVSCTGMYAPGLDIEIVQQLKLR
                                        TDAKRTAINFMGCYGAFNALKVAD
                                        DACRANKEAVVLVVSVELCSLHFQNDDDLDHLLS
                                        NAIFADGAAAALIQPMAENRKSLS
                                        IEAFNCDLLPQTSEDMAWHIVDSGFDIVLKSYIP
                                        EVIESGIAEFMEKLLKQEAITDVN
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                                        EYGNMSSATILFVLKELMTHLTSE
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                38)
CDS             complement(527278..5275 /locus-tag="Psyc-0422"
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gene            complement(527666..5280 /locus-tag="Psyc-0423"
                94)
CDS             complement(527666..5280 /locus-tag="Psyc-0423"
                94)
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                                        /db-xref="GI:71037978"
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                                        LIKDSDCEGYDSEALRAHIKQAGC
                                        FNNIPRKQNTKSTNNHMDWHLYKTRHLVENAFAK
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gene            528255..531563          /locus-tag="Psyc-0424"
CDS             528255..531563          /locus-tag="Psyc-0424"
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                                        /protein-id="AAZ18287.1"
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                                        HGLKIRNARFSLCQFKPEHSLNPETMTRYEANIC
                                        RVVSEVIYSPHVSLKDSPKDKTDG
                                        KVAKRNRIDIVLFVNGLPVTTMELKSEFKQAVQN
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                                        GTEHGGAGNDTPSDSSRYATDYLW
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                                     catalyse dimer splitting into the
                                     constituent monomers, a process
                                     called photoreactivation."
                                     /note="Citation: Sancar A, Smith
                                     FW, Sancar GB. 1984. Purification
                                     of Escherichia coli DNA
                                     photolyase. J Biol Chem.
                                     259(9):6028-32."
                                     /codon-start=1
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                                     KALRVNTEQDTLESVNMQIDNFAASGASSILLDA
                                     YHQHKYGGTGARFDWSLIPKDSSL
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                                     IYFKREDLNHTGAHKVNNTIGQALLAKMSGKKRI
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                                     IVYMGADDVERQKMNVYRMRLLGATVVPVTSGSR
                                     TLKDAMNEAMRDWVTNVDSTYYII
                                     GTVAGPHPYPLLVRDFQAIIGKEARIQHLQMTGK
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                                     DTEVKMYGVEATGDGIETGRHSAPLAAGRIGVLH
                                     GNRTYLMADDEGQIQETHSISAGL
                                     DYPGVGPEHSFLKDMKRVEYVGCTDKESLEGFHE
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CDS             542793..543629       /gene="trpA"
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                                     EALIVLYGKLRNLDIVTCAFDFRF
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                                     EAIGAEKAGILRDGISVIYGAAEM
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                                        variety of enzymes involved in
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                                        /note="Signal predicted by SignalP
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CDS             complement(548678..5496 /locus-tag="Psyc-0438"
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                                     KLGFASAWSSWVTATTNNSVSDIFDLLTGTEFDT
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                                     RSTFIQDASIDNAKIKNLDGDKITANTITASKLA
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gene                 complement(555447..5560 /locus-tag="Psyc-0444"
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CDS                  complement(555447..5560 /locus-tag="Psyc-0444"
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                                     VAVGVFVPGMQWAIGAGVGLMIGGAASLLMPTPN
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gene                 complement(556066..5568 /locus-tag="Psyc-0445"
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CDS                  complement(556066..5568 /locus-tag="Psyc-0445"
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                                     LambdaSo, tail assembly protein K"
                                     /protein-id="AAZ18308.1"
                                     /db-xref="GI:71038000"
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                                     HAVKDYKAPLINREYIHGVLDCFSIVRDYYSREL
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                                     DNFASQGFVQVDSLQRHDVILCRVQPTEHVNHAL
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gene            complement(556815..5576 /locus-tag="Psyc-0446"
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                                     RPSAPTLVIANKIDDTLGAVTAVCAFYNDFVGAT
                                     LTVTHVLAKYLDAANFAVGNPTAN
                                     PSESMTQYWYVEQKTEENEQTVTFELASPLSAQR
                                     KKIPTRNITPYCTWAVRGKYRGES
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gene            complement(557921..5590 /locus-tag="Psyc-0447"
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CDS             complement(557921..5590 /locus-tag="Psyc-0447"
                09)
                                     /function="Reverse transcriptase
                                     uses an RNA template to produce
                                     DNA, for integration into the host
                                     genome and exploitation of a host
                                     cell (strategy employed in the
                                     replication of retroid elements,
                                     such as the retroviruses and
                                     bacterial retrons)."
                                     /note="Within putative prophage."
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                                     DNA polymerase (Reverse
                                     transcriptase)"
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                                     KREIYAPAFRDCVVQYAIYLRVMP
                                     IFDKTFIDQSFACRTGLGTHKAAEYAQDALRRAG
                                     PNTYTLQLDIKKFFYSIDRPTLRK
                                     LLERKIKDKRLVDLMMLFADYPEPKGIPIGNLLS
                                     QMFALIYMNPVDHYATRVLKPAAG
                                     YCRYVDDFLLFGLTRAQALTYRKLLTDFVEQKLK
                                     LTLSRSTIANTKRGANFCGYRTWR
                                     SGRFIRKHSLYKTRKAVRANKLESVISHLAHASK
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gene            complement(559269..5596 /locus-tag="Psyc-0448"
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CDS             complement(559269..5596 /locus-tag="Psyc-0448"
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                                     LAFELSYFGHPKTEKMSVQKLNAK
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gene            complement(559678..5611 /locus-tag="Psyc-0449"
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CDS             complement(559678..5611 /locus-tag="Psyc-0449"
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                                     NFPKGNNNNALRDVNDTAVLYEGTGYLTAGKTGS
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                                     EVALGLTQTAGSFYVLRTSAKASALTSGATLATD
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gene            complement(561153..5614 /locus-tag="Psyc-0450"
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                                     TLNFEQFNNT"
gene            complement(561553..5618 /locus-tag="Psyc-0451"
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CDS             complement(561553..5618 /locus-tag="Psyc-0451"
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                                     /note="similar to Shewanella
                                     oneidensis hypothetical protein
                                     SO2991"
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gene            complement(562011..5650 /locus-tag="Psyc-0452"
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CDS             complement(562011..5650 /locus-tag="Psyc-0452"
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                                     tail tip protein"
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                                     LGAIFQDTSDKIGDFLSTGGGGMADFFENIAPQI
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                                     LSGLKLKANEAIAGGKVRGYTAEF
                                     AEVTQSLLGNDLKYFSALNDTYHKGTNSKHASGQ
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                                     QYGYSVKVLNEYANPSKNATGGHLHVSVYGQKAT
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                                     DVANTKLAQMQLTHDQEMQYAQQSEQTDAERIRN
                                     QYALERREIQLTIKMDKELRKAKI
                                     DALNQAEQLALDERRYAFESELRQLTSIGQSDLA
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                                     GTGANYSIAQQYKSRLDVIKAAEE
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                                     AGQQSFVMASAGLNMYEAWGDAMAEGATLSQKIA
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                                     GYQTGGFTATGRDSDPAGLVHANEFVANAPTTRK
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                                     DLDQDNFDKRAWAAASYSQMLIKQ
                                     SMKDPASAEFGSIRYVKASKEFPATICSQVNGKN
                                     SFNAYSGFKDYYLIPELGIYNIDD
                                     GTVEFKKAYNDFCILK"
gene            complement(565850..5660 /locus-tag="Psyc-0454"
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CDS             complement(565850..5660 /locus-tag="Psyc-0454"
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gene            complement(566176..5665 /locus-tag="Psyc-0455"
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CDS             complement(566176..5665 /locus-tag="Psyc-0455"
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                                     AFEKAAFGADSEFKDYPQRAVTFAHAVVDENGKR
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                                     YNEINGVGPDKVEAAEKNS"
gene            complement(566615..5670 /locus-tag="Psyc-0456"
                37)
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                                        TTTV"
gene            complement(567059..5674 /locus_tag="Psyc_0457"
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CDS             complement(567059..5674 /locus_tag="Psyc_0457"
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                                        PDLYRQTADIRIWGTIF"
gene            complement(567436..5679 /locus_tag="Psyc_0458"
                03)
CDS             complement(567436..5679 /locus_tag="Psyc_0458"
                03)
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                                        prophage"
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                                        protein"
                                        /protein_id="AAZ18321.1"
                                        /db_xref="GI:71038013"
                                        /translation="MSNDLMNIEFEVLGLSELDN
                                        ALAELTLSMQKKTLEGALMKAALP
                                        IMKAAKKNANKSEAAHQLKYNDGQTFTIQPGTLK
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                                        GKPYPYYWHFVERGNSRMVATPYLRPAFEQNVEL
                                        AIQLFSEELTKRIDKLTQD"
gene            complement(567896..5682 /locus_tag="Psyc_0459"
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CDS             complement(567896..5682 /locus_tag="Psyc_0459"
                28)
                                        /codon_start=1
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                                        /db_xref="GI:71038014"
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                                        TEDDYGDTISSFGEVSQTFCEWLP
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gene            complement(568230..5685 /locus_tag="Psyc_0460"
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CDS             complement(568230..5685 /locus_tag="Psyc_0460"
                38)
                                        /codon_start=1
                                        /transl_table=11
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gene            complement(568652..5699 /locus-tag="Psyc-0461"
                05)
                                        /note="Signal predicted by SignalP
                                        2.0 HMM (Signal peptide probabilty
                                        0.922) with cleavage site
                                        probability 0.637 at residue 24"
CDS             complement(568652..5699 /locus-tag="Psyc-0461"
                05)
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                                        /transl-table=11
                                        /product="possible major phage
                                        capsid subunit precursor"
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                                        /translation="MRDIKKTALVCAIASMGVVT
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                                        DPNSIGGLLSRNEGISQEIKAIKHSRGKVQIDGV
                                        SARNTVLLGTINTAGNINDAKMVA
                                        ATEDPLTIVTMINWIPTTAPLIPYVRESAVTFMA
                                        DIVPEGMLKPESSLTFGVDSLEID
                                        VIAHWIQVSNQVLDDAPALAAYIEGRMAYGVRLK
                                        LEYLVINGDTKSFKGLMKVGNSLT
                                        IVSNDNAIDTISTAKAKAYANFLPPETVILNPQD
                                        WAGIEQVKGTDGHYIFGSPGAAVQ
                                        PVLWGLKVMQSPAMAIGKFWAGNITMATEGYIRQ
                                        DVTVELSTEDSDNFRKNLVTIRAE
                                        MRAAFGVVMPDAAVTGDLVNVGPVV"
gene            complement(569983..5707 /locus-tag="Psyc-0462"
                29)
CDS             complement(569983..5707 /locus-tag="Psyc-0462"
                29)
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                                        Unknown type peptidase. MEROPS
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                                        /protein-id="AAZ18325.1"
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                                        MRVGRWVEFEEDDIGLRVKGELTQGLPLATAVGA
                                        MMRHLTVDGLSICFYNPTEMDYEE
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gene            complement(570722..5719 /locus-tag="Psyc-0463"
                57)
CDS             complement(570722..5719 /locus-tag="Psyc-0463"
                57)
                                        /function="it forms the junction
                                        between the phage head (capsid)
                                        and the tail proteins"
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                                        /transl-table=11
                                        /product="probable phage portal
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                                        /protein-id="AAZ18326.1"
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                                        LMLNLVSDGNAYVRITRIGEKNSRIISLDIINSS
                                        NMTVILKNDELIYRHQITSAFSRD
                                        FKESDIWHVKLFGNGIKGLSPLQHATKAVAVADA
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                                        AISLTPSDIELLATRRFSLEEIAR
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gene            complement(571959..5737 /locus-tag="Psyc-0464"
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CDS             complement(571959..5737 /locus-tag="Psyc-0464"
                04)
                                     /function="Terminases cleave the
                                     cohesive ends of lambda family
                                     phage."
                                     /note="Often located next to the
                                     small subunit."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="probable phage
                                     terminase, large subunit"
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                                     AARSGWLNMQDWDDAADKTLVAGLFDKYPCFGGL
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                                     DMQETGYDPFNATYLAMRLNEQGLNMVEVPQRVA
                                     YLSEPMKHLQALLTSKRVHHDGNP
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                                     SQLGDYLTDFVSFRG"
gene            complement(573711..5741 /locus-tag="Psyc-0465"
                84)
CDS             complement(573711..5741 /locus-tag="Psyc-0465"
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                                     /function="Terminases cleave the
                                     cohesive ends of lambda family
                                     phage."
                                     /note="Members tend to be adjacent
                                     to the phage terminase large
                                     subunit gene."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="possible phage
                                     terminase, small subunit"
                                     /protein-id="AAZ18328.1"
                                     /db-xref="GI:71038020"
                                     /translation="MARPRKPTQLKVLQGSRVRS
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gene            complement(574289..5747 /locus-tag="Psyc-0466"
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                                     protein"
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gene            complement(574862..5752 /locus_tag="Psyc_0467"
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CDS             complement(574862..5752 /locus_tag="Psyc_0467"
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                                     NEIGNKKLAARWWETKHRKIAKSEVAKDLDVMMA
                                     VEAQSMFQRYFLIYGTKEVWDDVE
                                     RIRLPVDTIKLARPNEYEIWLKSEARITIKADNI
                                     WFDPTRTKSPKHDKDIAINTFDGL
                                     PLKPIETELSDAAAMCKPITDLLLHLCEGSKEVY
                                     EWVLRWLAIPLQQPGTKLDTALIF
                                     HGEIQGAGKSLFFDRVMTRIYGDYAVTLGQGQLD
                                     SSYNDWVSDKLYALFEEIFSGNDS
                                     HSQMGMVKQLITGNTIYISKKFMSGWQQDNFVNA
                                     VFLSNNMKPLSLEQNDRRHVVCYP
                                     QQKIPEPILNDVATALTDADAKMLRAFYTLLMLT
                                     DLKDQTAHTPAIITASKNQLIRLS
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                                     WCHRNGERPTTETKVMTYIGRREH
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                                     RAQSIWDNAKPAADDHPYLLRKNV
                                     SAIGLSQDANDNLIIPMYYHNADKQQITLVNVQT
                                     IAPDSDKLFLKGGLVSGAYFTIGS
                                     PAMFSAGIILICEGYATGATVFDAMSYSLPVIVA
                                     FNAHNLIPVTQSIRAQYPDHRIII
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gene            complement(579064..5793 /locus-tag="Psyc-0471"
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CDS             complement(579064..5793 /locus-tag="Psyc-0471"
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gene            579446..580120       /locus-tag="Psyc-0472"
CDS             579446..580120       /locus-tag="Psyc-0472"
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                                        the protein becomes covalently
                                        linked to the DNA through a
                                        catalytic tyrosine residue at the
                                        carboxy end of the alignment."
                                        /note="Within putative prophage."
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                                        TAKEVRTLIADIIWSSEKTRNNNLIPLRGVFGIA
                                        LDDSVIHTNPVDKIKNTKHQSPPP
                                        DPFSRDEMERLLTWLHDKHGKDEAVYWLYFELAF
                                        WTGMRTGELLALTWDDIDWDAGLI
                                        KVSKVMSDGELVNRTKTAEYRDVFFNARSEDALK
                                        RLKRIKSAVSDRLFMSPRFINSAW
                                        QTDKTPRRALTEAMKATGIRHRATYTTRHTFITN
                                        CLTDGLNIYFVAKQTGHSVRTLET
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tRNA            complement(585389..5854 /locus-tag="Psyc-R0017"
                65)
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gene            complement(585580..5871 /gene="gatB"
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                                        /function="-This enzyme functions
                                        as an alternative to a direct
                                        Gln-tRNA synthetase (Gln--tRNA
                                        ligase) in mitochondria,
                                        chloroplasts, gram-positive
                                        bacteria, cyanobacteria, and the
                                        Archaea."
                                        /codon-start=1
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                                        NYFYPDLPKGYQITQMANPIVGEGYIDVVVNEGE
                                        KNEYPKRMGITRAHLEEDAGKSVH
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                                        AYIKAIHQLVTWLGISDAIMAEGS
                                        FRCDCNVSIRKPGAELGTRTELKNLNSFRFIERA
                                        INREIERQIDILEDGGKVVQATML
                                        YDPERDETRVMRTKEDANDYRYFPDPDLLPVRIE
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                                        KMAANWVMGDLLGALNKDDKDIID
                                        SPISAKQLAGMLARIKDDTLSGKLAKKVFGALYE
                                        RAGGDADDAADKIIEEKGLKQETD
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                                        A"
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                                        YDATIVTNIDKAGMISLGKLNMDEFAMGSDNESS
                                        YYGAVHNPWNIGHVPGGSSGGSAA
                                        AVAAGFVPVATGSDTGGSIRQPASFCGLTGIKPT
                                        YGRVSRFGMIAYASSLDQAGSMGR
                                        SAMDCAYLLQPMIGHDPRDATSIKYDMPDYVQDL
                                        NDAAASAGDKPFAGLRIGVAKEYF
                                        SKGLDTEVEQAARAALKKYEELGATIVEVTITDP
                                        EITLATYYMLAPAEASSNLSRFDG
                                        VRFGYRCENPKDLIDLYTRSRSEGFGPEVQRRIL
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                                        IVKDFEDAFANCDVIASPTAPTAAYKLGEDLDPA
                                        TMYLGDVYTIGVNLAGLPALSQPV
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                                        /EC-number="6.3.5.-"
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                                        /transl-table=11
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                                        C"
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gene            589699..590727          /gene="mreB"
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=> log h
COST IN U.S. DOLLARS                            SINCE FILE      TOTAL
                                                     ENTRY    SESSION
FULL ESTIMATED COST                                 184.40     192.54

 SESSION WILL BE HELD FOR 120 MINUTES
STN INTERNATIONAL SESSION SUSPENDED AT 09:45:35 ON 12 MAR 2009
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